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Wilson, Jr. et al.

(10) **Patent No.: US 12,281,148 B2**
(45) **Date of Patent: *Apr. 22, 2025**

(54) **ANTI-PD-1 ANTIBODY-ATTENUATED IL-2 IMMUNOCONJUGATES AND USES THEREOF**

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(73) Assignee: **Cephalon LLC**

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

This patent is subject to a terminal disclaimer.

(21) Appl. No.: **18/823,422**

(22) Filed: **Sep. 3, 2024**

(65) **Prior Publication Data**

US 2024/0425562 A1 Dec. 26, 2024

Related U.S. Application Data

(63) Continuation of application No. 18/335,650, filed on Jun. 15, 2023.

(Continued)

(51) **Int. Cl.**
C07K 14/55 (2006.01)
C07K 16/28 (2006.01)

(52) **U.S. Cl.**
CPC ***C07K 14/55*** (2013.01); ***C07K 16/2818*** (2013.01); *C07K 2317/21* (2013.01);
(Continued)

(58) **Field of Classification Search**
CPC C07K 14/55; C07K 16/2818; C07K 2317/21; C07K 2317/75; C07K 2317/92; C07K 2319/33; C07K 2319/75
See application file for complete search history.

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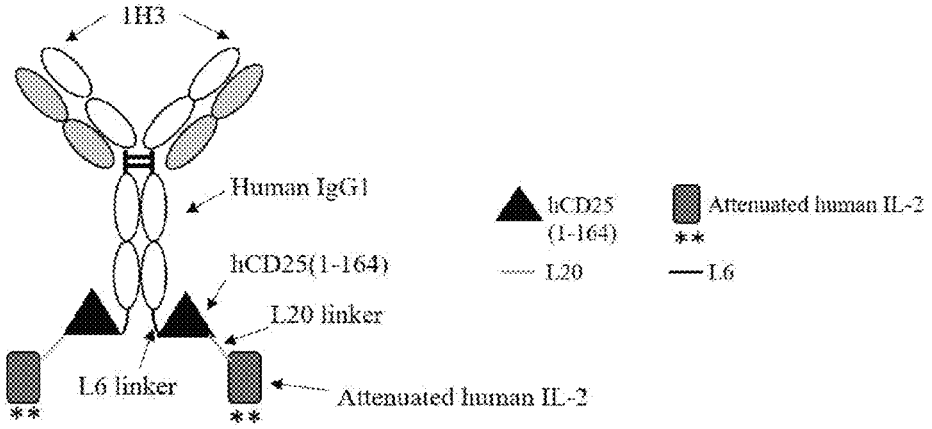
Assistant Examiner — Laura Ann Essex
(74) *Attorney, Agent, or Firm* — BakerHostetler

(57) **ABSTRACT**

Disclosed herein are modified human interleukin-2 (hIL-2) proteins, human antibody molecules, or antigen-binding fragments thereof, that immunospecifically bind to human programmed cell death protein-1 (hPD-1), and immunoconjugates comprising the same.

10 Claims, 26 Drawing Sheets

Specification includes a Sequence Listing.



1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2

Related U.S. Application Data

(60) Provisional application No. 63/502,746, filed on May 17, 2023, provisional application No. 63/481,630, filed on Jan. 26, 2023, provisional application No. 63/352,842, filed on Jun. 16, 2022.

(52) **U.S. Cl.**
CPC *C07K 2317/75* (2013.01); *C07K 2317/92* (2013.01); *C07K 2319/33* (2013.01); *C07K 2319/75* (2013.01)

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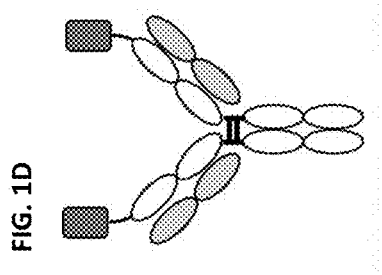


FIG. 1A

hIL-2 Nterm light chain df

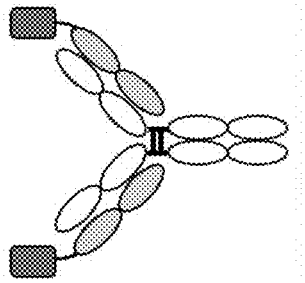


FIG. 1B

hIL-2 Nterm light chain L6 fusion

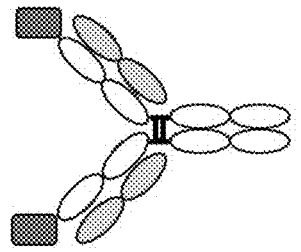


FIG. 1C

hIL-2 Nterm heavy chain df

FIG. 1D

hIL-2 Nterm heavy chain L6 fusion

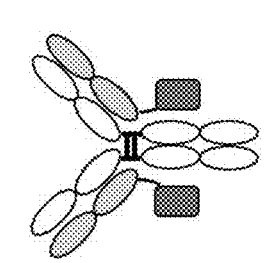


FIG. 1E

hIL-2 Cterm heavy chain df

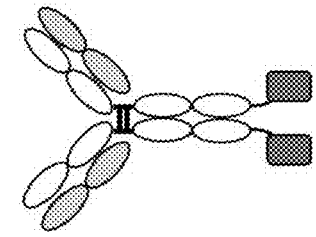


FIG. 1F

hIL-2 Cterm heavy chain L6 fusion

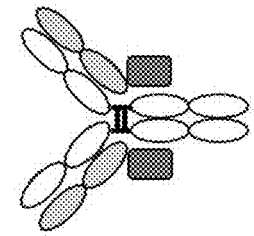


FIG. 1G

hIL-2 Cterm light chain df

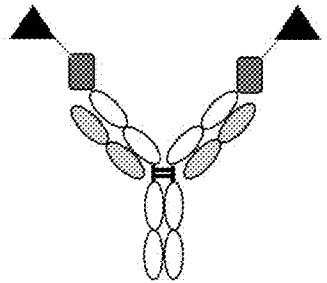
FIG. 1H

hIL-2 Cterm light chain L6 fusion

hIL-2

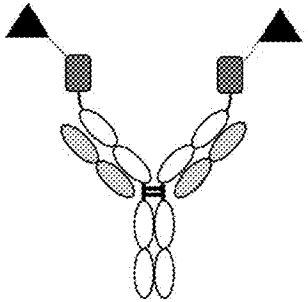
L6

FIG. 2A



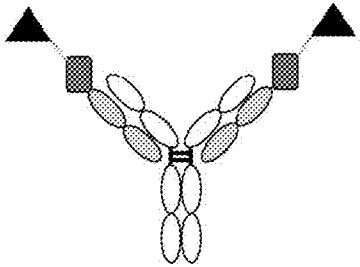
hCD25-L20-hIL-2 Nterm heavy chain df

FIG. 2B



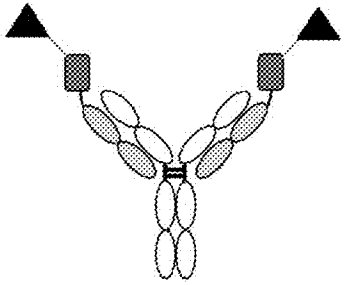
hCD25-L20-hIL-2 Nterm heavy chain L6 fusion

FIG. 2C



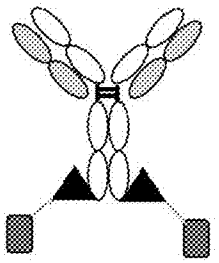
hCD25-L20-hIL-2 Nterm light chain df

FIG. 2D



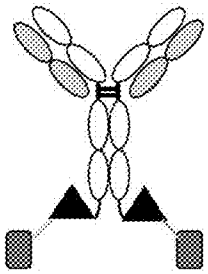
hCD25-L20-hIL-2 Nterm light chain L6 fusion

FIG. 2E



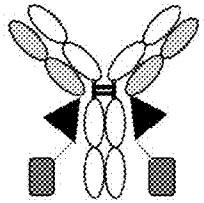
hCD25-L20-hIL-2 Cterm heavy chain df

FIG. 2F



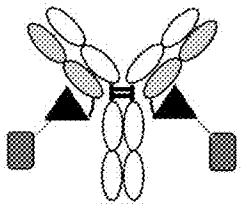
hCD25-L20-hIL-2 Cterm heavy chain L6 fusion

FIG. 2G

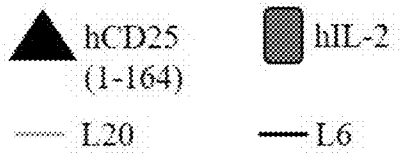


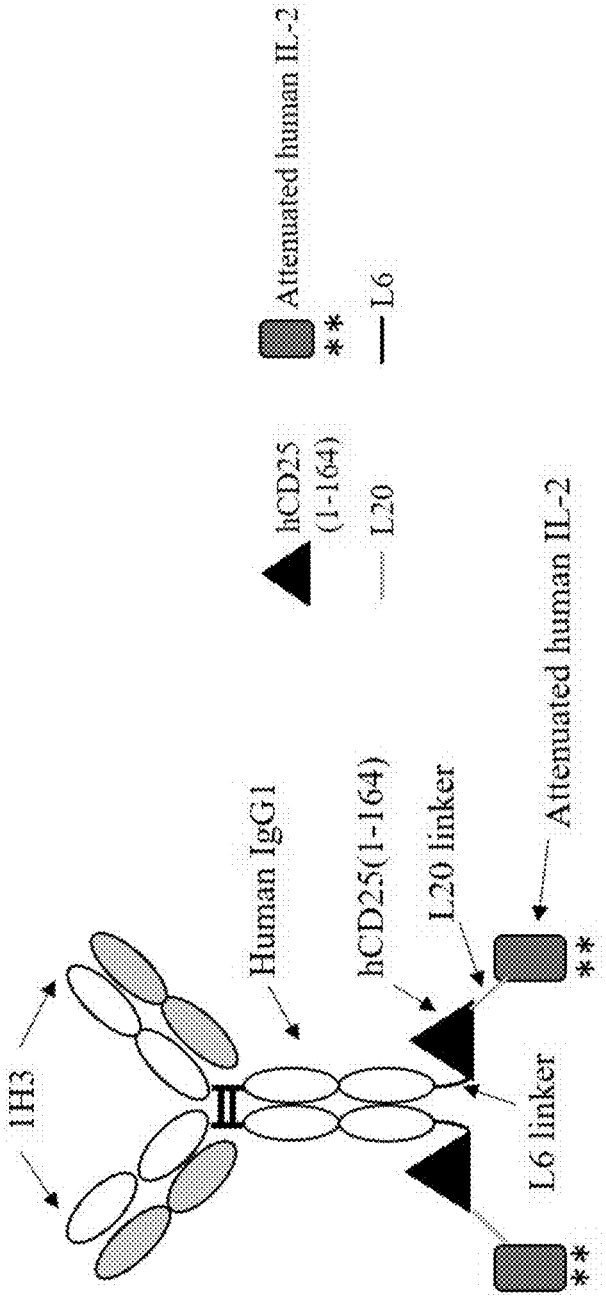
hCD25-L20-hIL-2 Cterm light chain df

FIG. 2H



hCD25-L20-hIL-2 Cterm light chain L6 fusion





1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2

FIG. 3

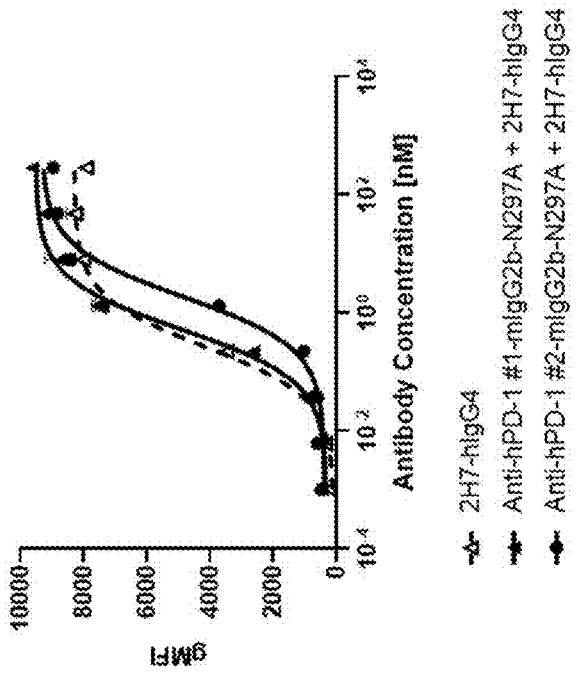

gMFI
10000
8000
6000
4000
2000
0
10^{-4}
10^{-2}
10^{0}
10^{2}
10^{4}
Antibody Concentration [nM]
2H7-hIgG4
Anti-hPD-1 #1-mIgG2b-N297A + 2H7-hIgG4
Anti-hPD-1 #2-mIgG2b-N297A + 2H7-hIgG4

FIG. 4B

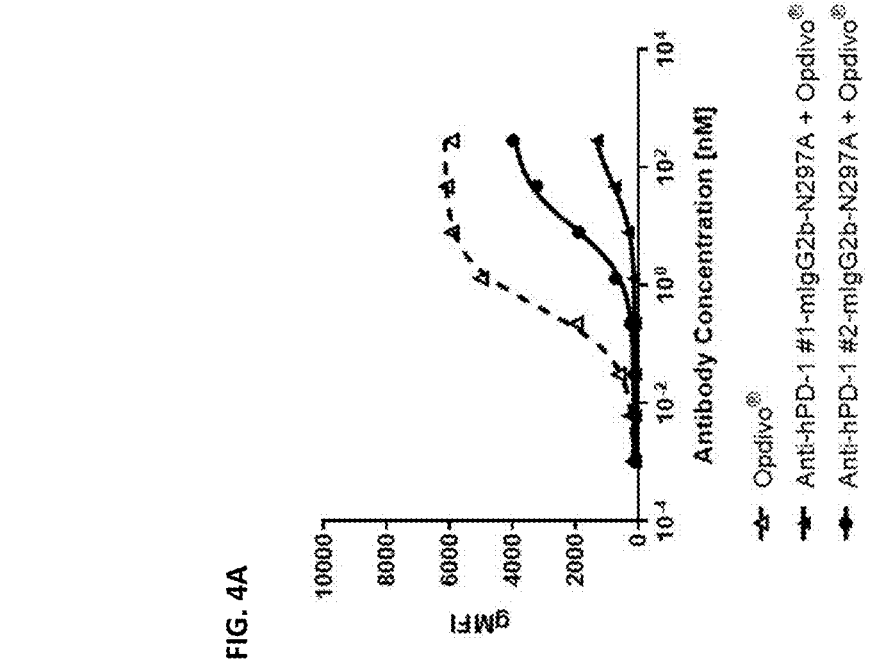

gMFI
10000
8000
6000
4000
2000
0
10^{-4}
10^{-2}
10^{0}
10^{2}
10^{4}
Antibody Concentration [nM]
Opdivo®
Anti-hPD-1 #1-mIgG2b-N297A + Opdivo®
Anti-hPD-1 #2-mIgG2b-N297A + Opdivo®

FIG. 4A

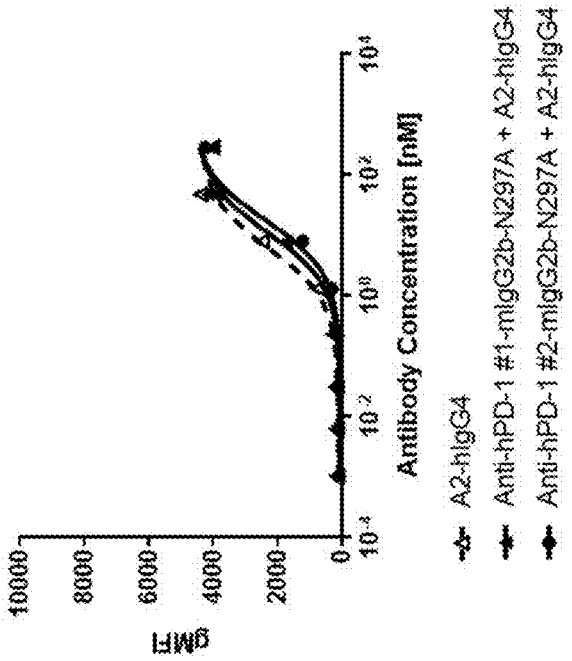

gMFI
10000
8000
6000
4000
2000
0
10^{-4}
10^{-2}
10^{0}
10^{2}
10^{4}
Antibody Concentration [nM]
A2-hIgG4
Anti-hPD-1 #1-mIgG2b-N297A + A2-hIgG4
Anti-hPD-1 #2-mIgG2b-N297A + A2-hIgG4

FIG. 4D

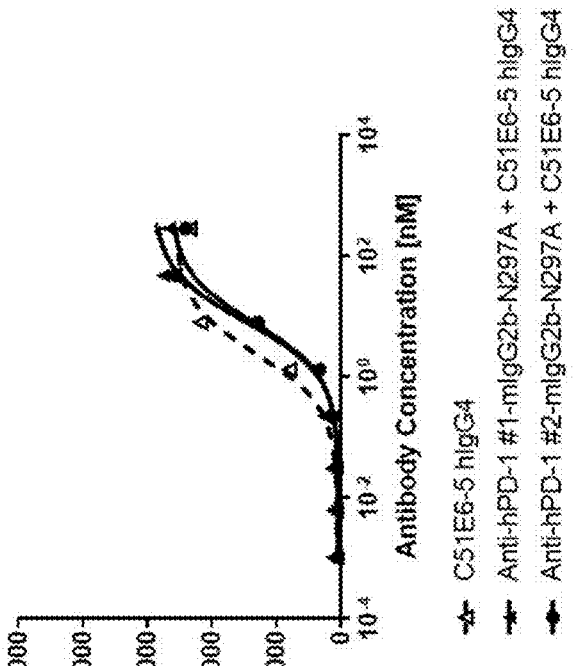

gMFI
10000
8000
6000
4000
2000
0
10^{-4}
10^{-2}
10^{0}
10^{2}
10^{4}
Antibody Concentration [nM]
C51E6-5 hIgG4
Anti-hPD-1 #1-mIgG2b-N297A + C51E6-5 hIgG4
Anti-hPD-1 #2-mIgG2b-N297A + C51E6-5 hIgG4

FIG. 4C

FIG. 5

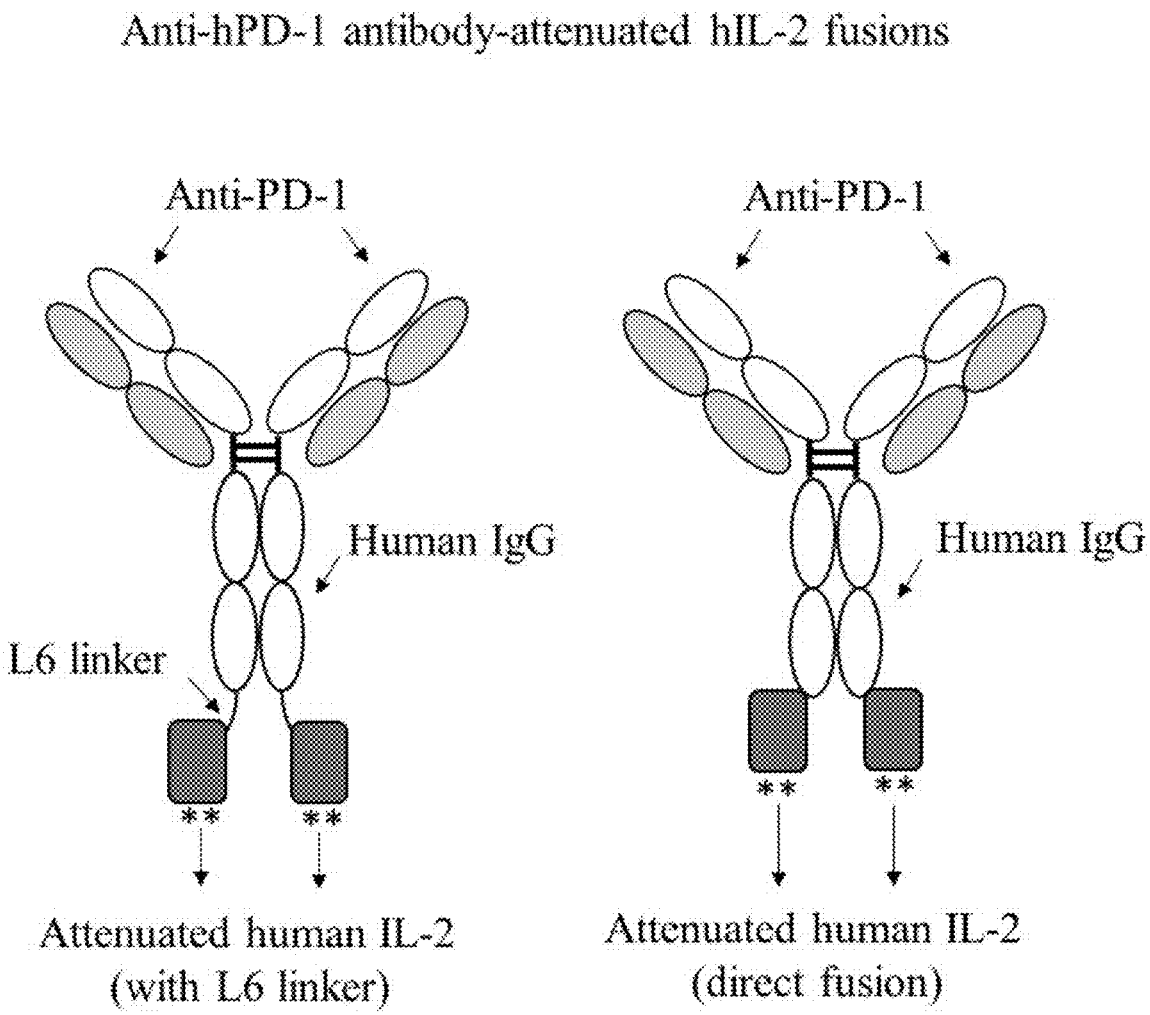
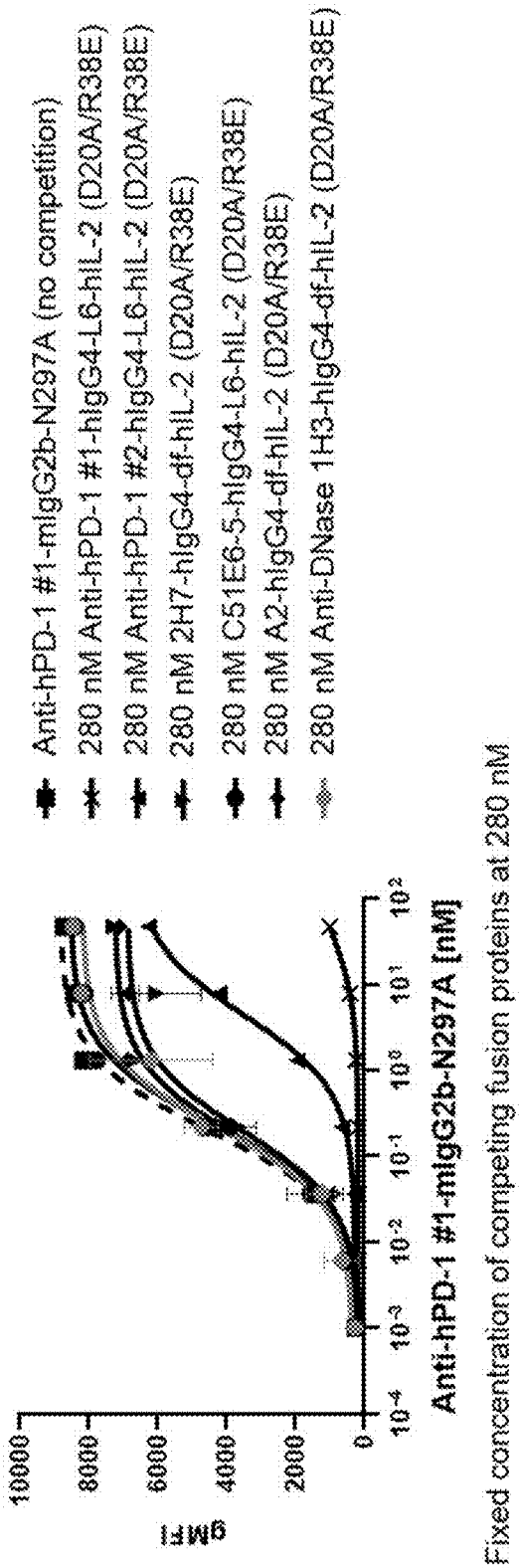

Anti-hPD-1 antibody-attenuated hIL-2 fusions
Anti-PD-1
Human IgG
L6 linker
**
**
Attenuated human IL-2
(with L6 linker)
Anti-PD-1
Human IgG
**
**
Attenuated human IL-2
(direct fusion)

FIG. 6A


Anti-hPD-1 #1-mIgG2b-N297A (no competition)
280 nM Anti-hPD-1 #1-hIgG4-L6-hIL-2 (D20A/R38E)
280 nM Anti-hPD-1 #2-hIgG4-L6-hIL-2 (D20A/R38E)
280 nM 2H7-hIgG4-df-hIL-2 (D20A/R38E)
280 nM C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E)
280 nM A2-hIgG4-df-hIL-2 (D20A/R38E)
280 nM Anti-DNase 1H3-hIgG4-df-hIL-2 (D20A/R38E)
gMFI
10000
8000
6000
4000
2000
0
10^{-4}
10^{-3}
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
Anti-hPD-1 #1-mIgG2b-N297A [nM]
Fixed concentration of competing fusion proteins at 280 nM

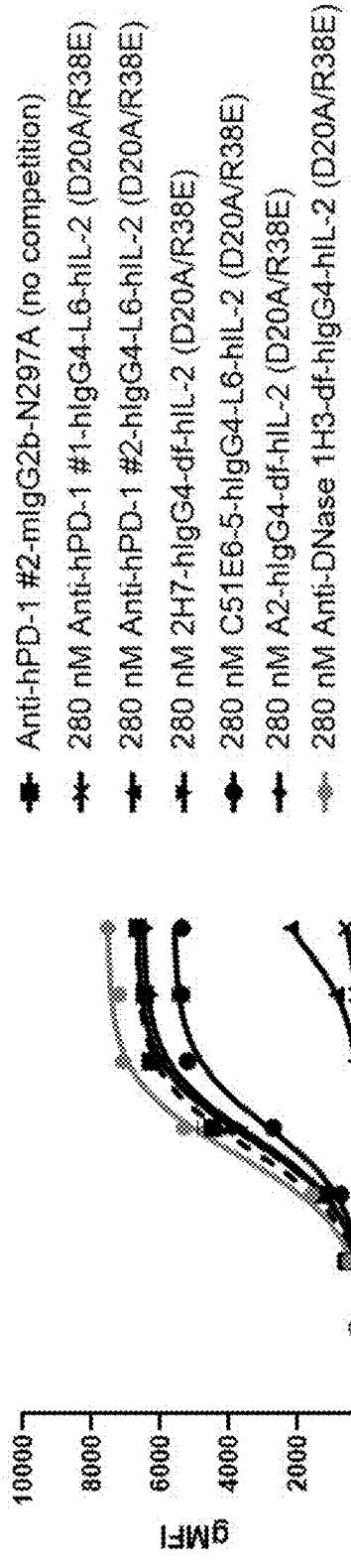

Anti-hPD-1 #2-mIgG2b-N297A (no competition)
280 nM Anti-hPD-1 #1-hIgG4-L6-hIL-2 (D20A/R38E)
280 nM Anti-hPD-1 #2-hIgG4-L6-hIL-2 (D20A/R38E)
280 nM 2H7-hIgG4-df-hIL-2 (D20A/R38E)
280 nM C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E)
280 nM A2-hIgG4-df-hIL-2 (D20A/R38E)
280 nM Anti-DNase 1H3-df-hIgG4-hIL-2 (D20A/R38E)
gMFI
10000
8000
6000
4000
2000
0
10^{-4}
10^{-3}
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
Anti-hPD-1 #2-mIgG2b-N297A [nM]
Fixed concentration of competing fusion proteins at 280 nM

FIG. 6B

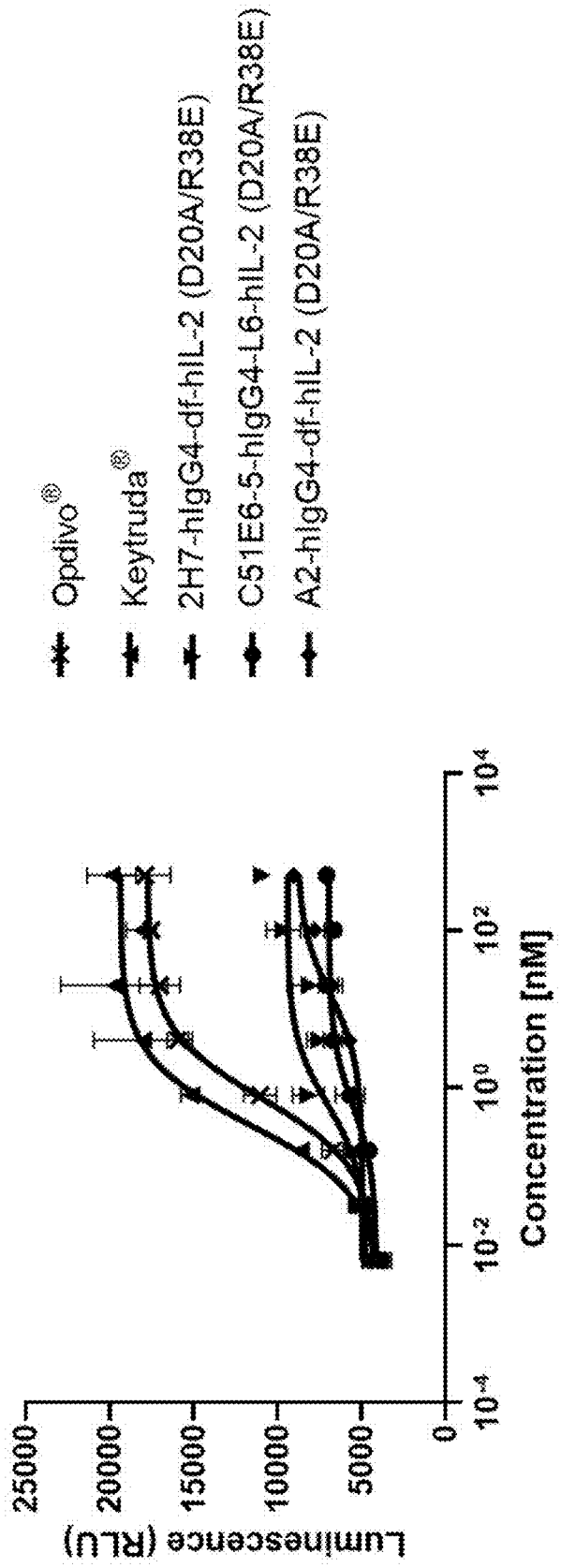

Opdivo®
Keytruda®
2H7-hIgG4-df-hIL-2 (D20A/R38E)
C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E)
A2-hIgG4-df-hIL-2 (D20A/R38E)
Luminescence (RLU)
25000
20000
15000
10000
5000
0
10-4
10-2
100
102
104
Concentration [nM]

FIG. 7

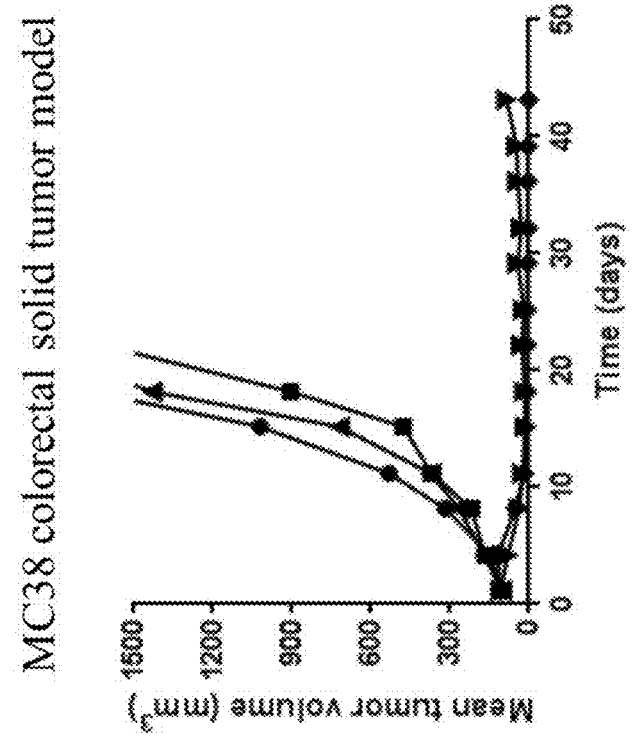

MC38 colorectal solid tumor model
Mean tumor volume (mm3)
1500
1200
900
600
300
0
0
10
20
30
40
50
Time (days)
Vehicle
Anti-mPD-1 RMP1-14 mIgG2b-N297A
Anti-mPD-1 RMP1-30 mIgG2b-N297A
Anti-mPD-1 RMP1-14 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)
Anti-mPD-1 RMP1-30 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)

FIG. 8

FIG. 9A

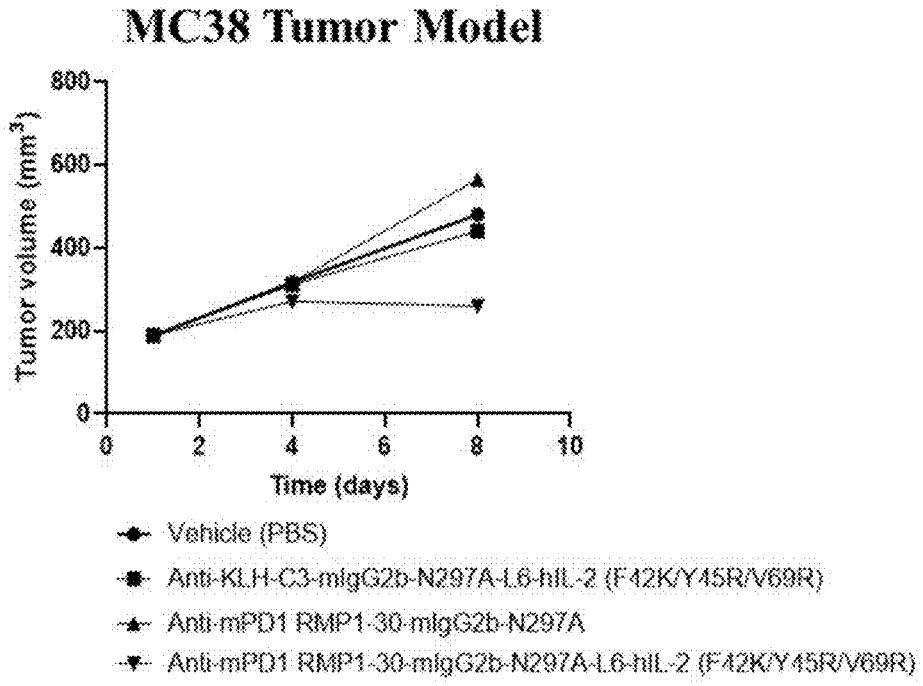

MC38 Tumor Model
Tumor volume (mm3)
800
600
400
200
0
0
2
4
6
8
10
Time (days)
Vehicle (PBS)
Anti-KLH-C3-mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)
Anti-mPD1 RMP1-30-mIgG2b-N297A
Anti-mPD1 RMP1-30-mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)

FIG. 9B

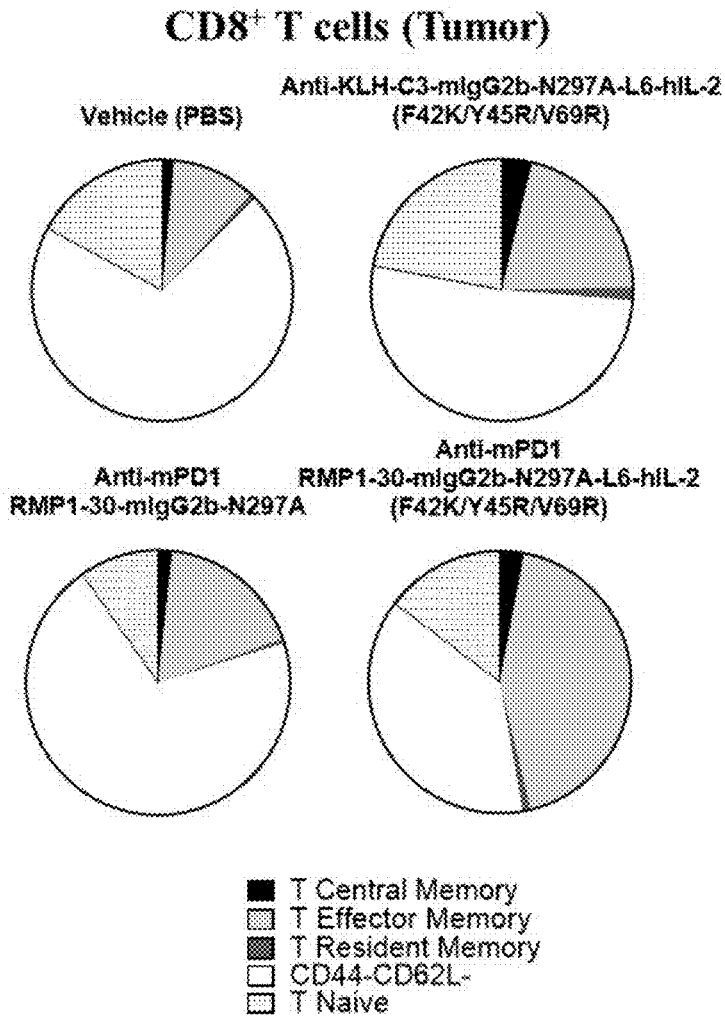
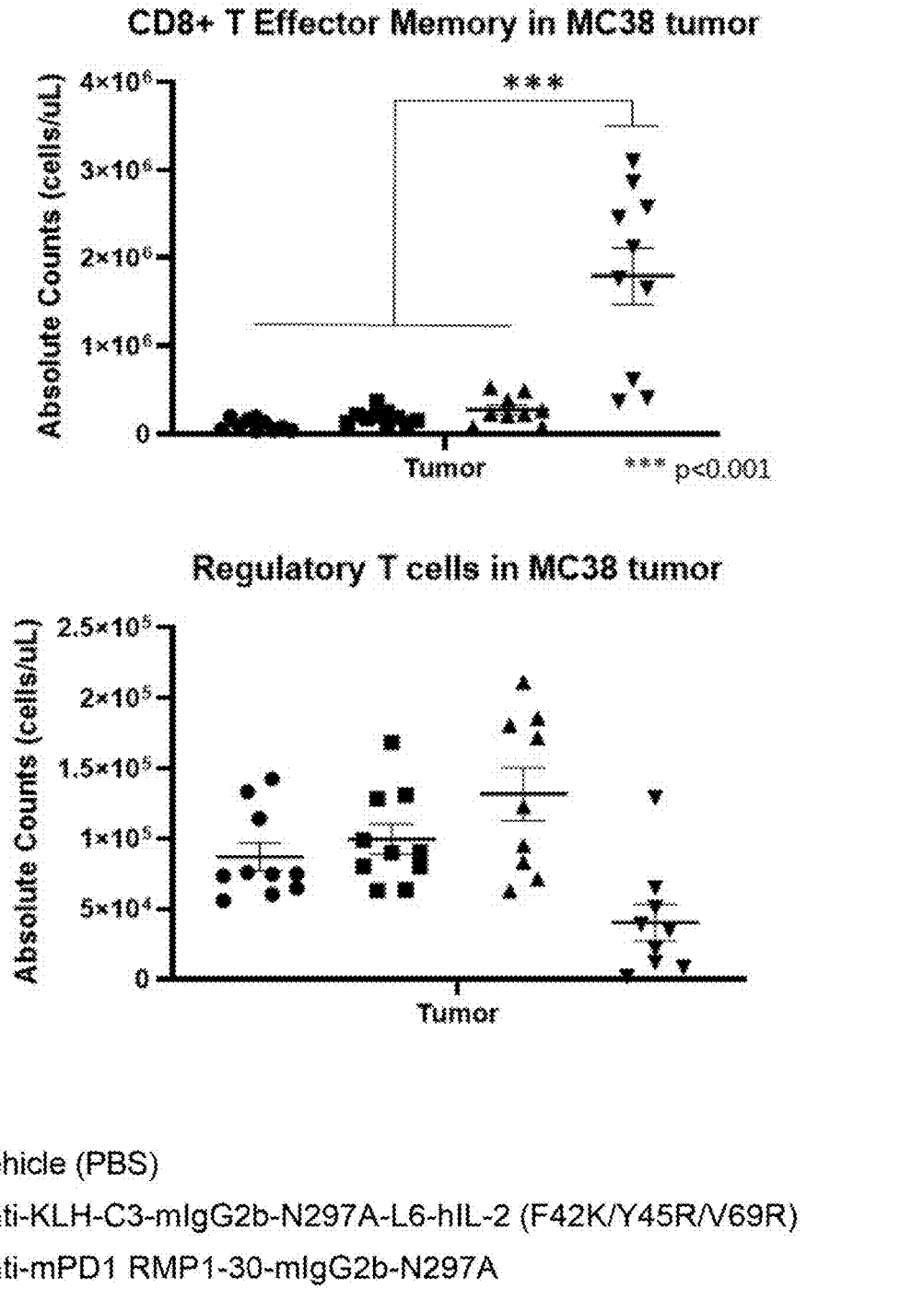

CD8+ T cells (Tumor)
Vehicle (PBS)
Anti-KLH-C3-mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)
Anti-mPD1 RMP1-30-mIgG2b-N297A
Anti-mPD1 RMP1-30-mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)
T Central Memory
T Effector Memory
T Resident Memory
CD44-CD62L-
T Naive

FIG. 9C


CD8+ T Effector Memory in MC38 tumor
Absolute Counts (cells/uL)
4×10^6
3×10^6
2×10^6
1×10^6
0
***
Tumor
*** p<0.001
Regulatory T cells in MC38 tumor
Absolute Counts (cells/uL)
2.5×10^5
2×10^5
1.5×10^5
1×10^5
5×10^4
0
Tumor
Vehicle (PBS)
Anti-KLH-C3-mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)
Anti-mPD1 RMP1-30-mIgG2b-N297A
Anti-mPD1 RMP1-30-mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)

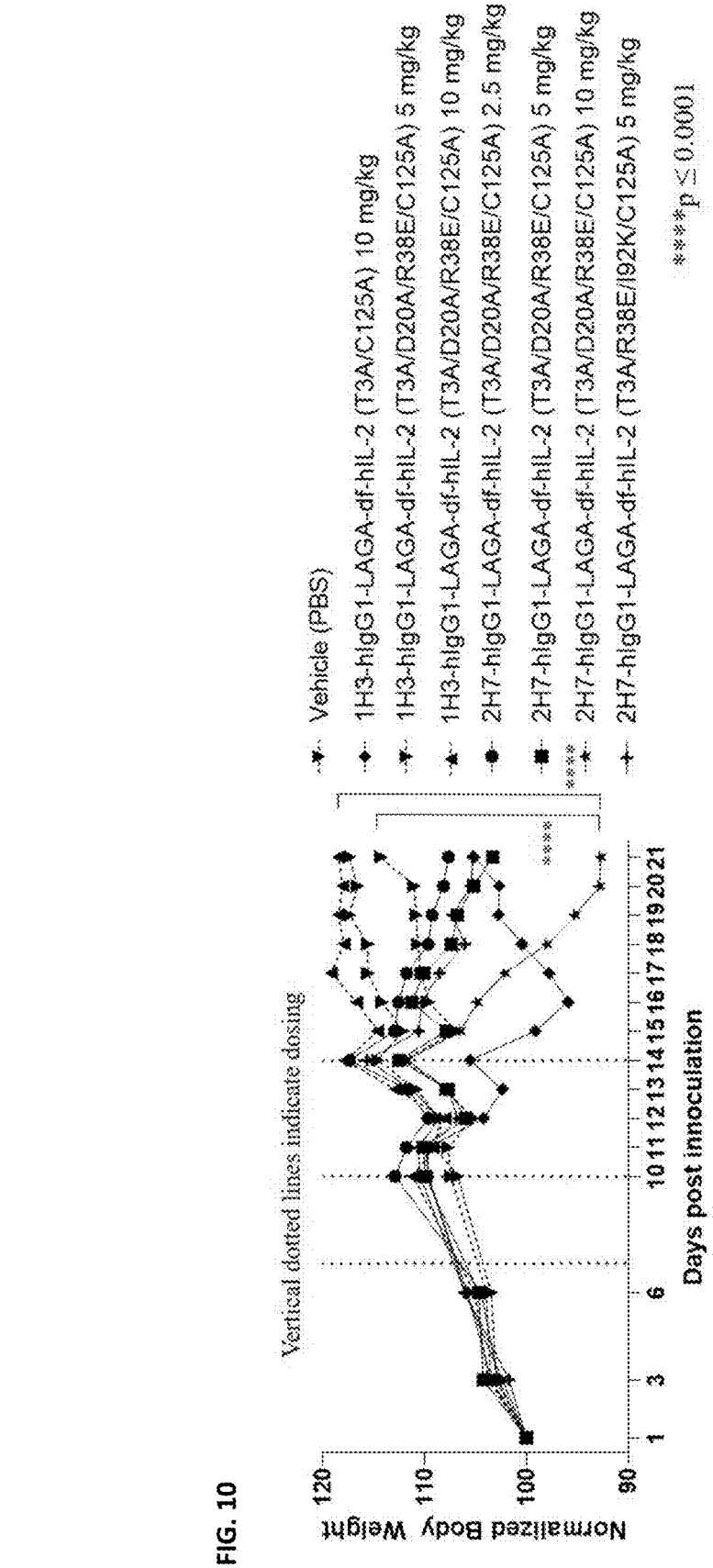

Normalized Body Weight
120
110
100
90
1
3
6
10 11 12 13 14 15 16 17 18 19 20 21
Days post innoculation
Vertical dotted lines indicate dosing
****
****
Vehicle (PBS)
1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A) 10 mg/kg
1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 5 mg/kg
1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 10 mg/kg
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 2.5 mg/kg
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 5 mg/kg
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 10 mg/kg
2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A) 5 mg/kg
****p ≤ 0.0001

FIG. 10

FIG. 11B

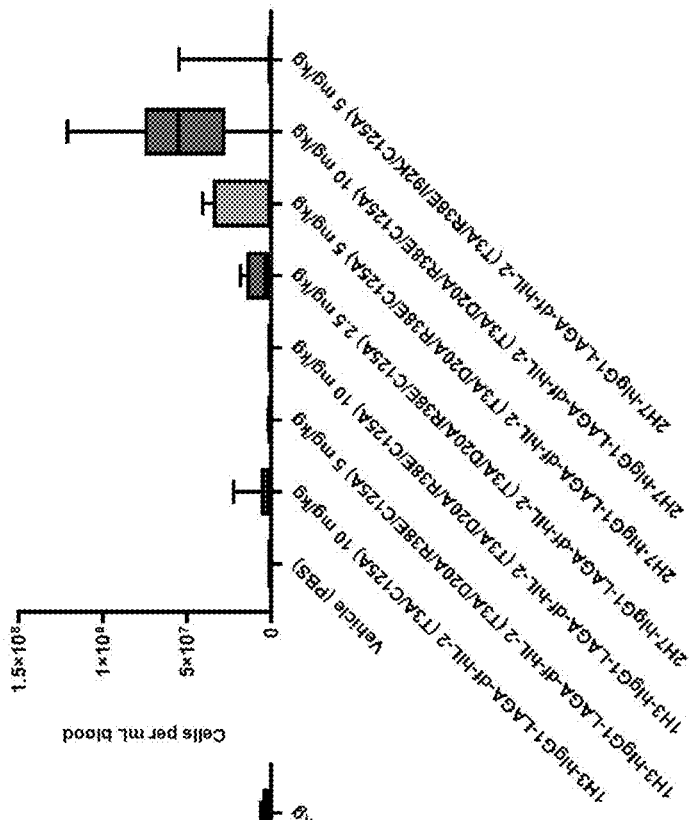


FIG. 11A

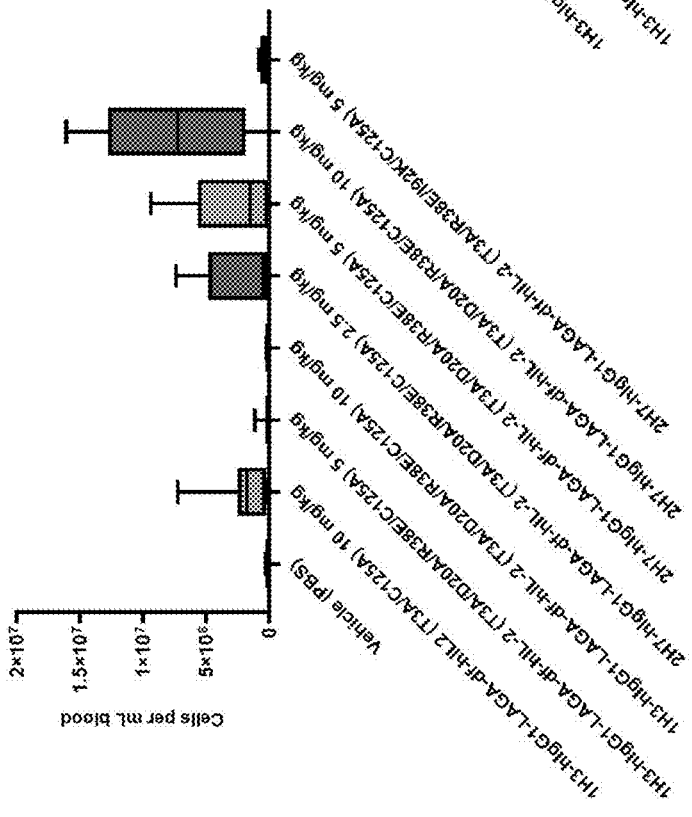


FIG. 12

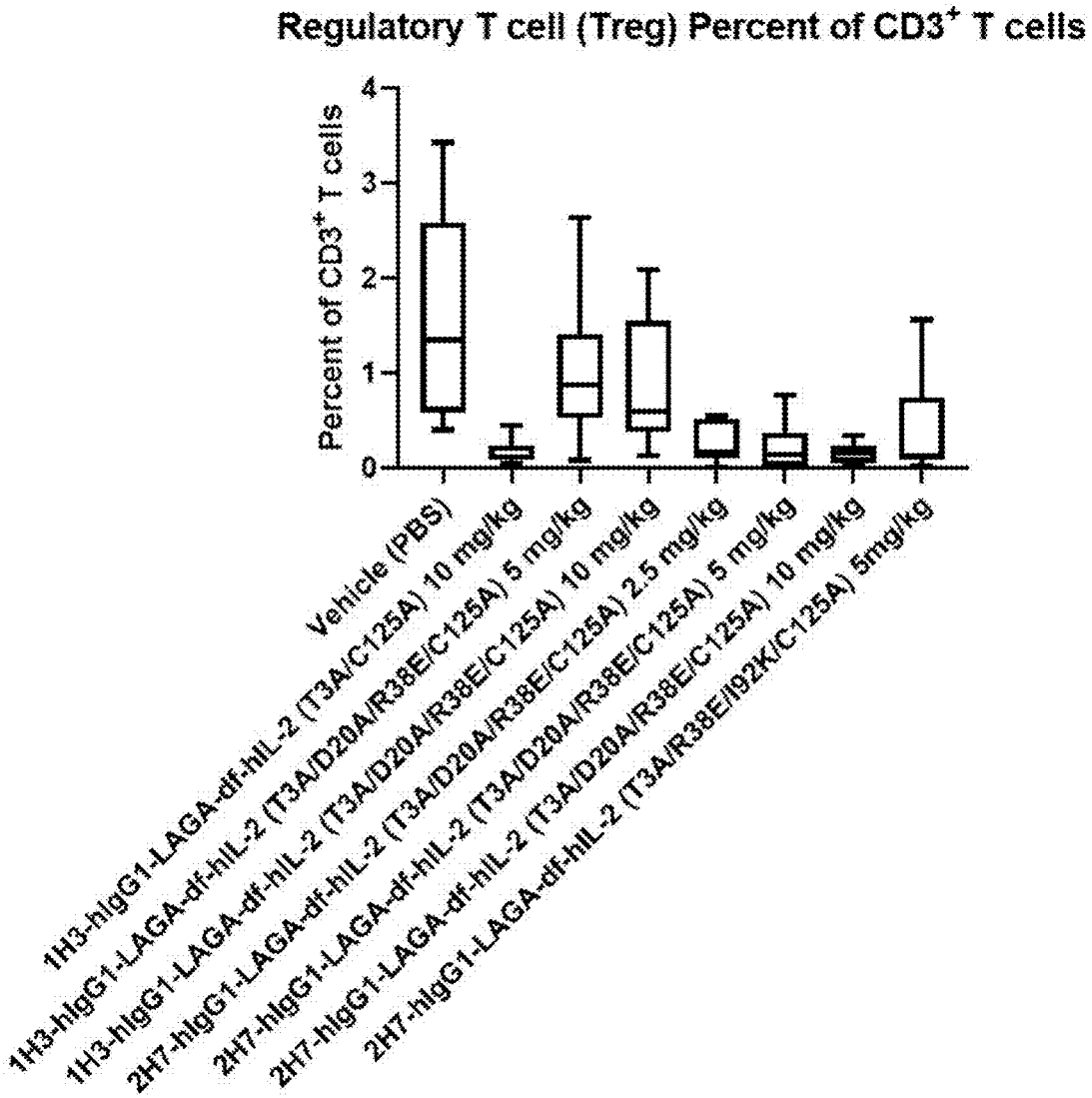

Regulatory T cell (Treg) Percent of CD3+ T cells
Percent of CD3+ T cells
0
1
2
3
4
Vehicle (PBS)
1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A) 10 mg/kg
1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 5 mg/kg
1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 10 mg/kg
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 2.5 mg/kg
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 5 mg/kg
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 10 mg/kg
2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A) 5mg/kg

FIG. 13B

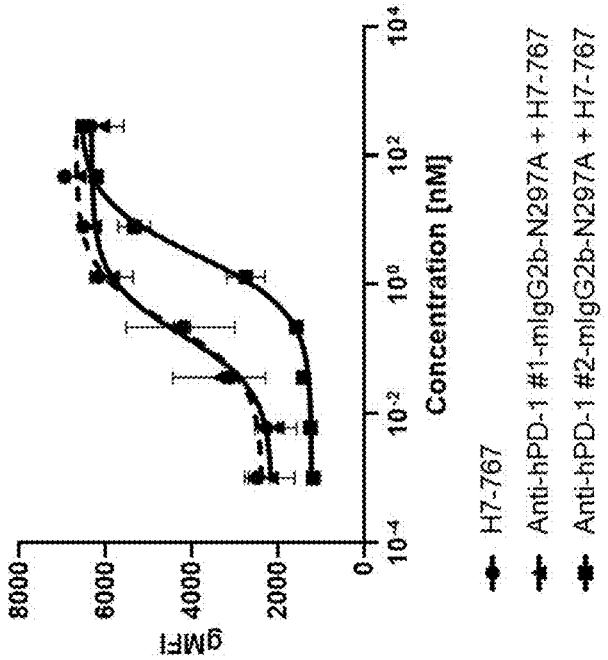
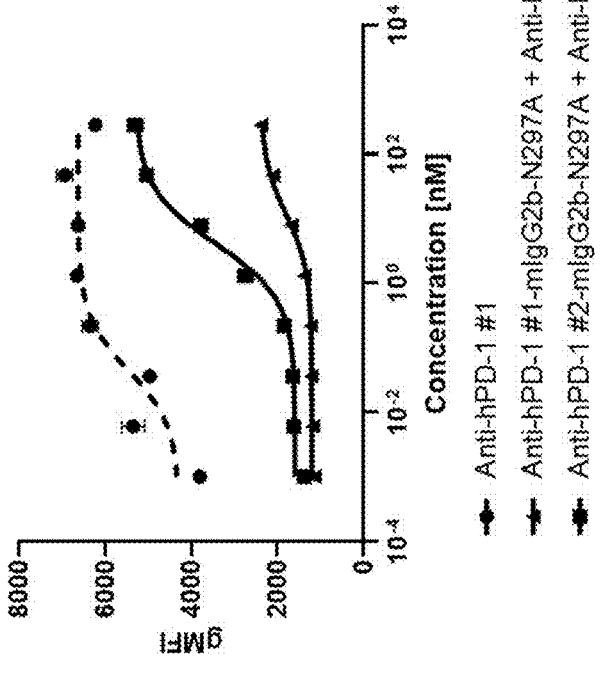


FIG. 13A



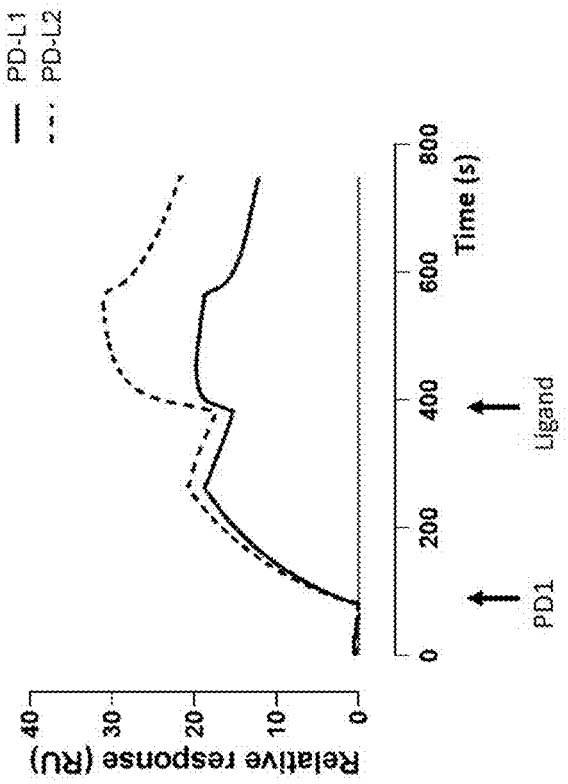


FIG. 14B

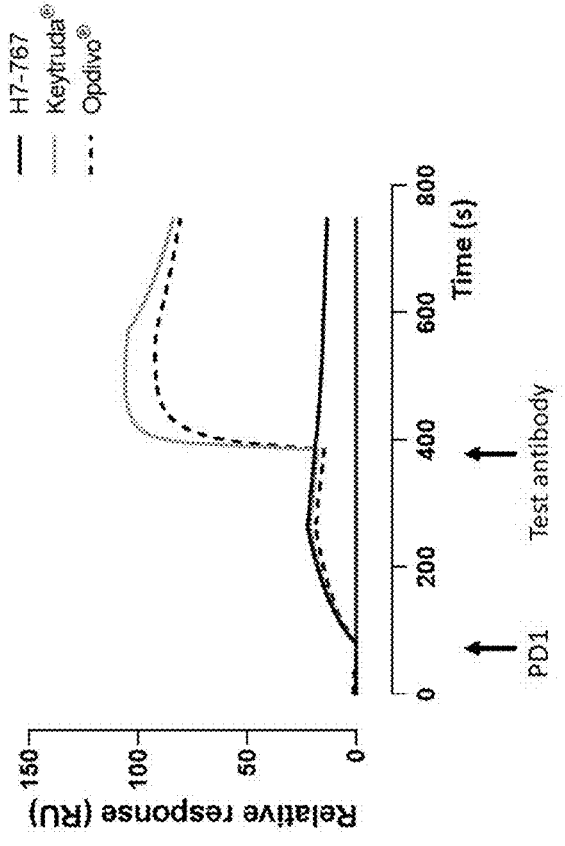


FIG. 14A

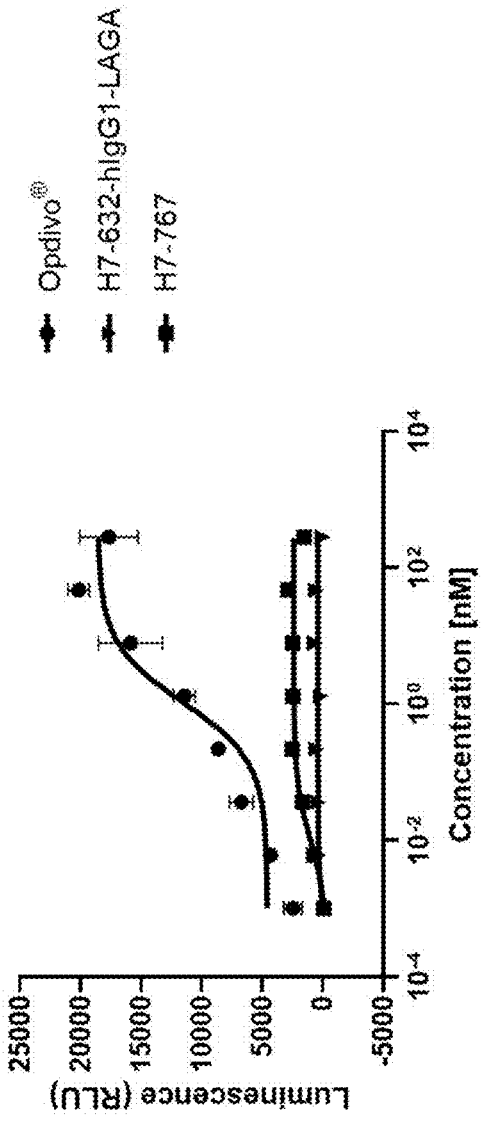

Opdivo®
H7-632-hIgG1-LAGA
H7-767
Luminescence (RLU)
25000
20000
15000
10000
5000
0
-5000
10⁻⁴
10⁻²
10⁰
10²
10⁴
Concentration [nM]

FIG. 15

FIG. 16B

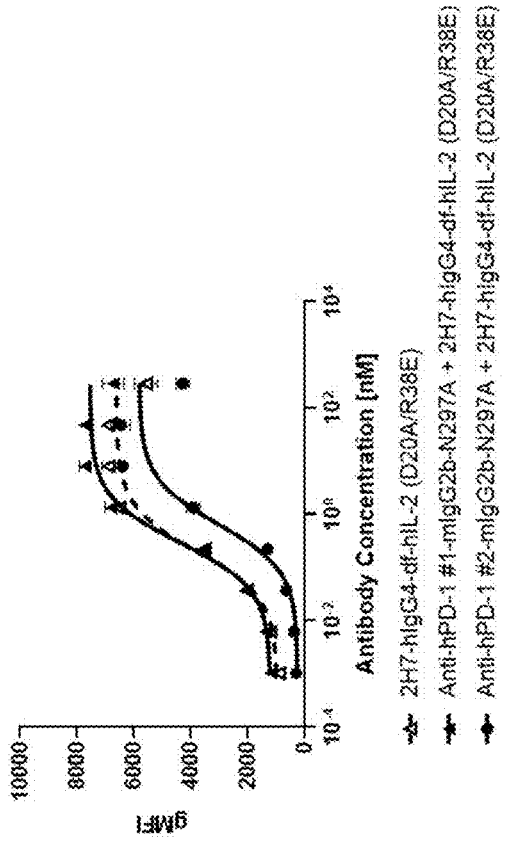


FIG. 16A

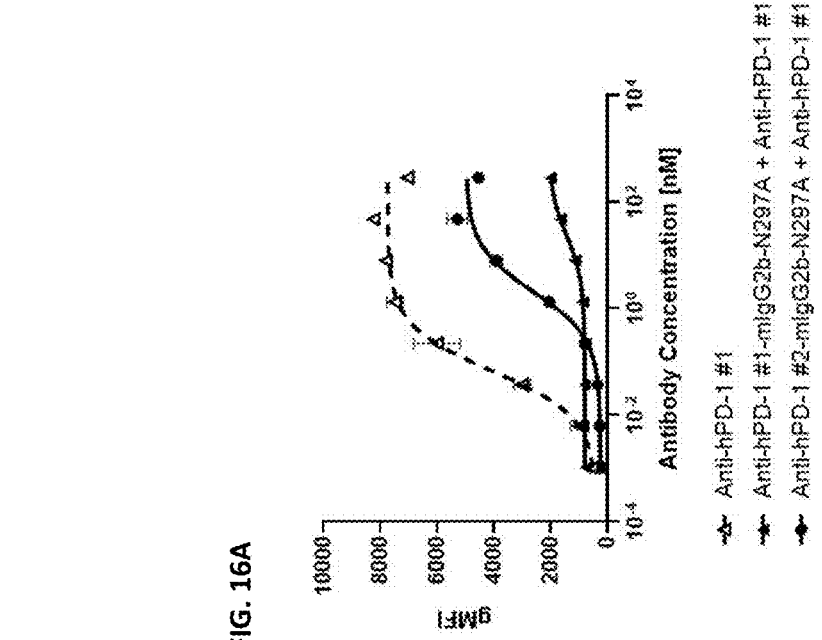


FIG. 16C

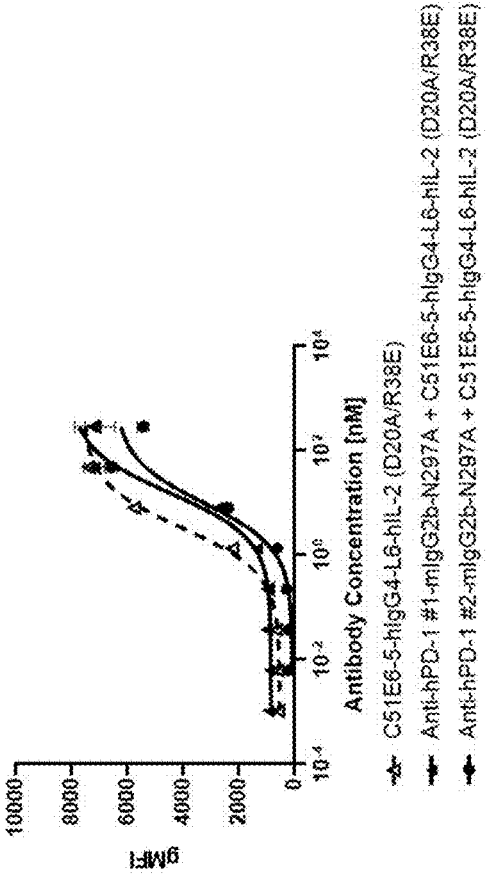
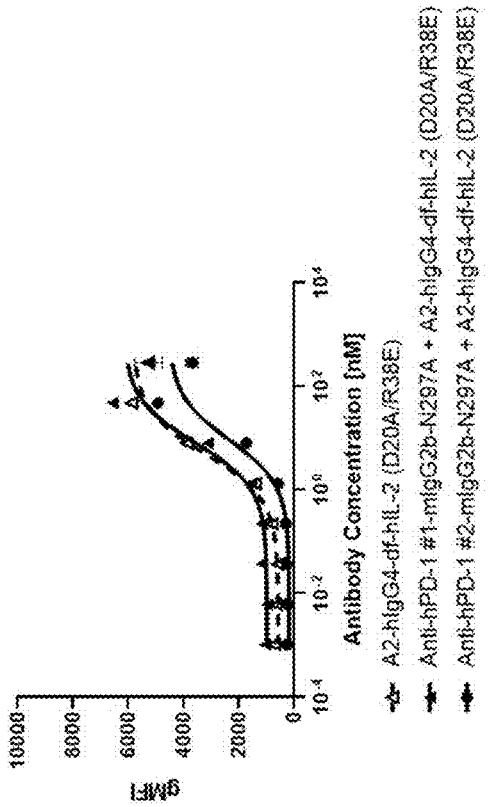


FIG. 16D



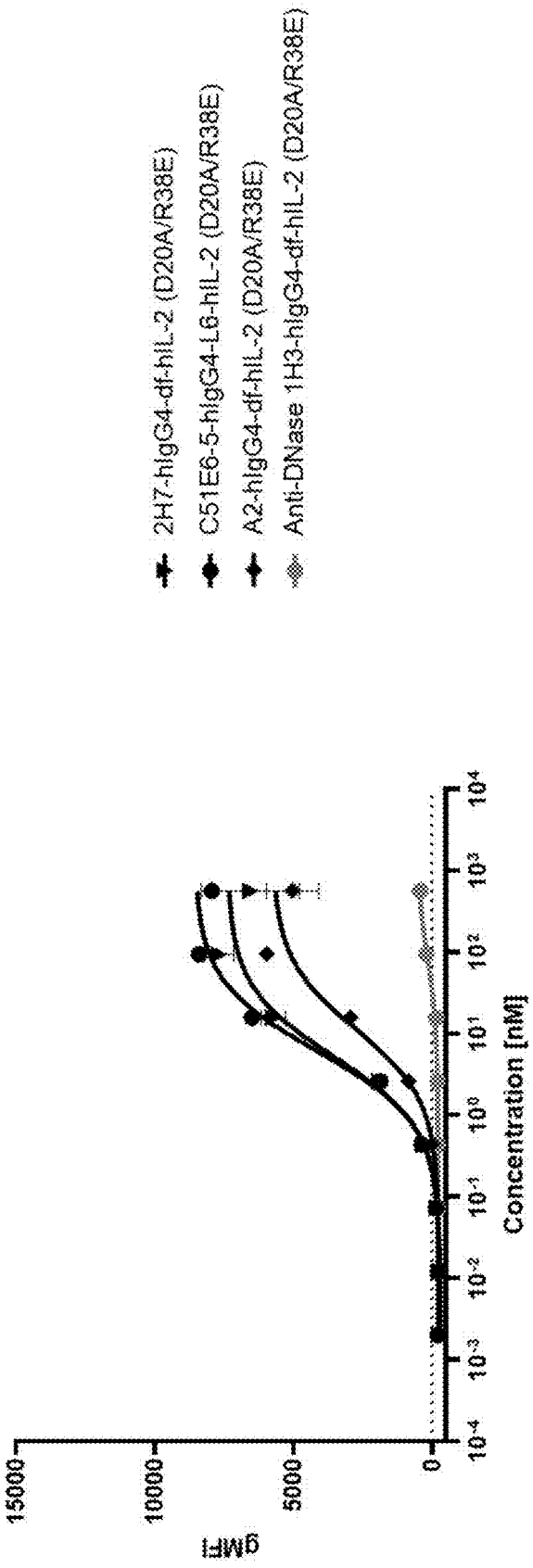

2H7-hIgG4-df-hIL-2 (D20A/R38E)
C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E)
A2-hIgG4-df-hIL-2 (D20A/R38E)
Anti-DNase 1H3-hIgG4-df-hIL-2 (D20A/R38E)
gMFI
15000
10000
5000
0
10^{-4}
10^{-3}
10^{-2}
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}
Concentration [nM]

FIG. 17

FIG. 18A

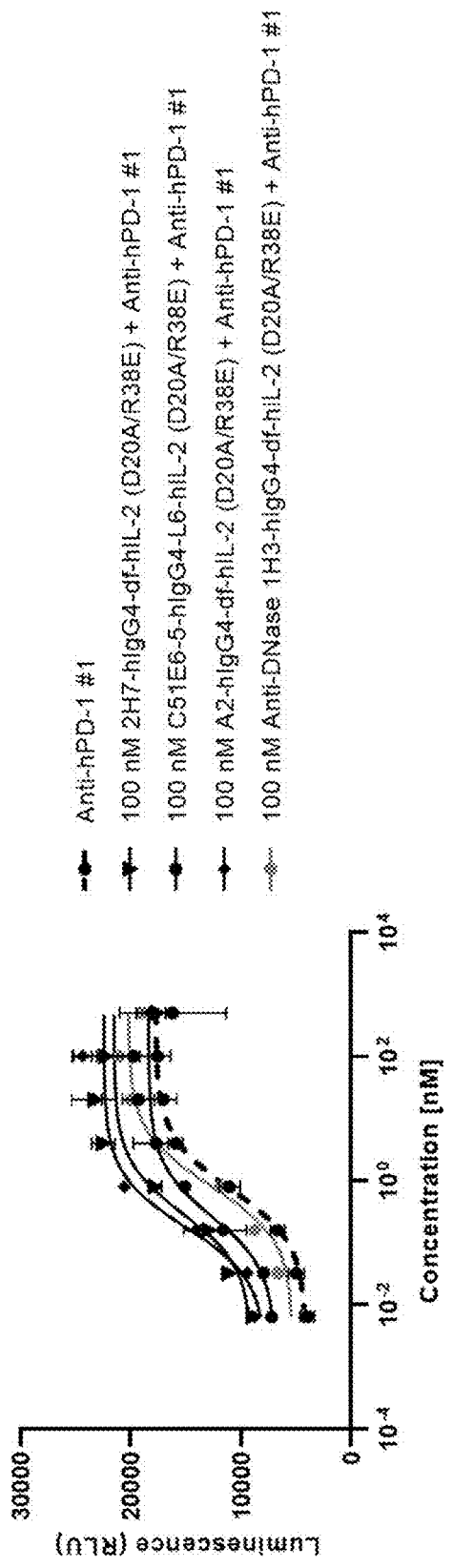
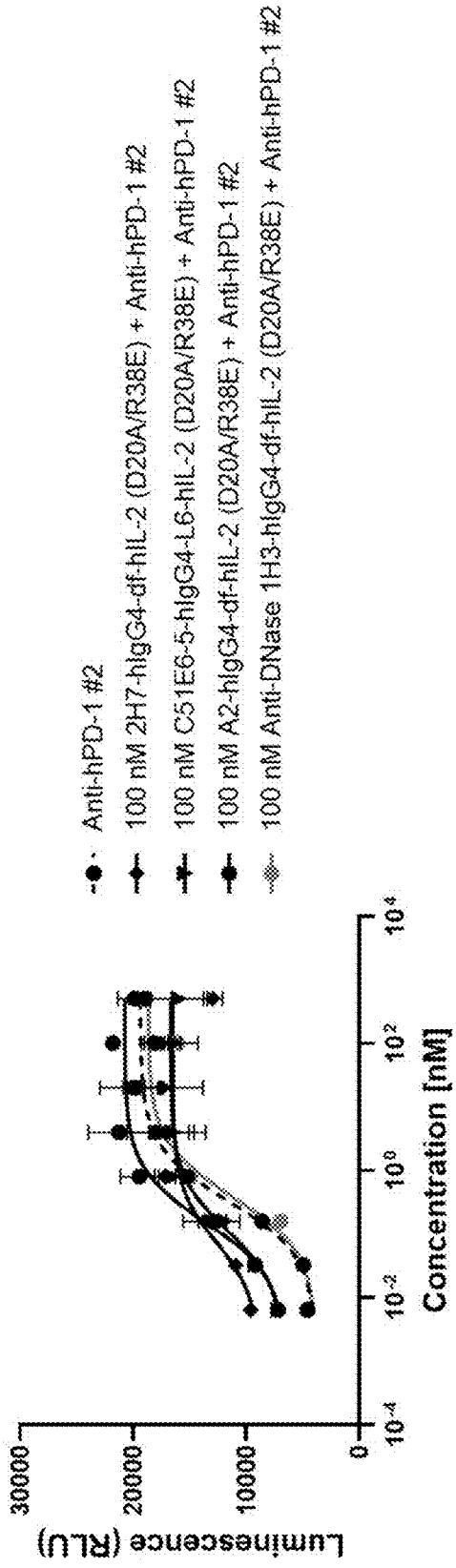


FIG. 18B



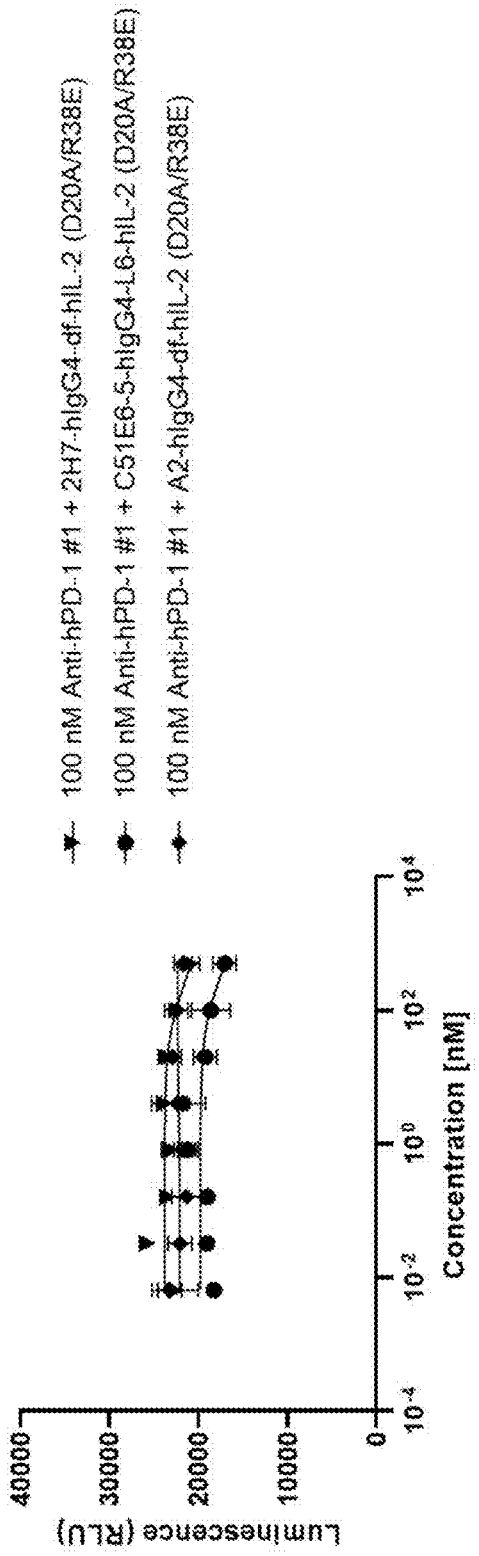


FIG. 18C

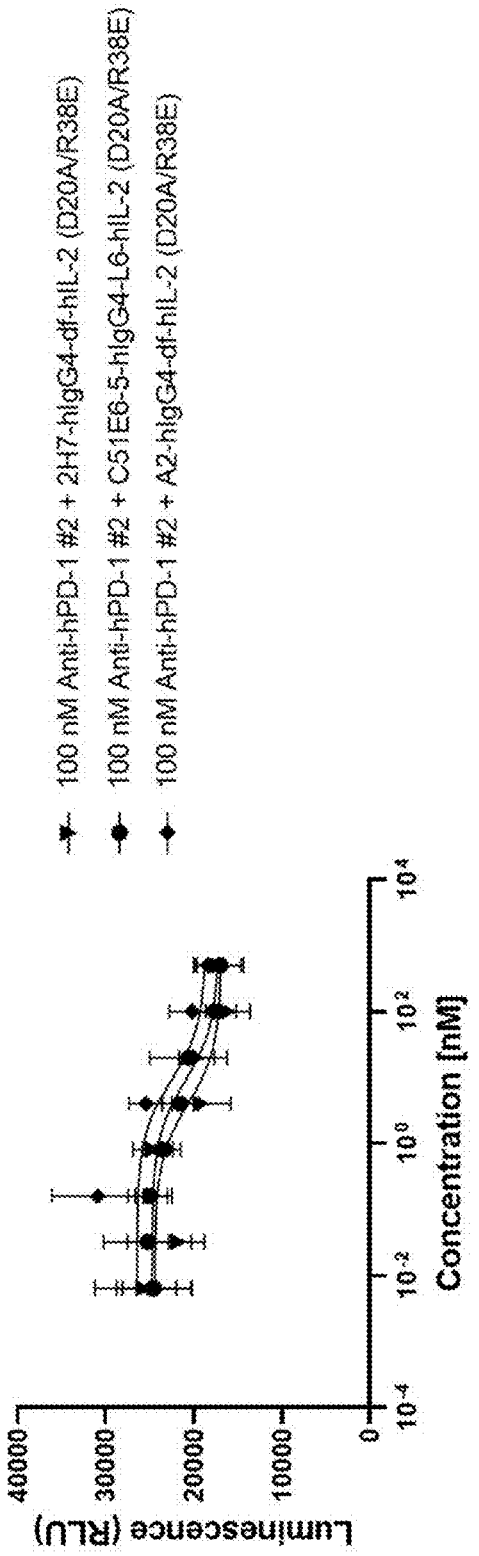


FIG. 18D

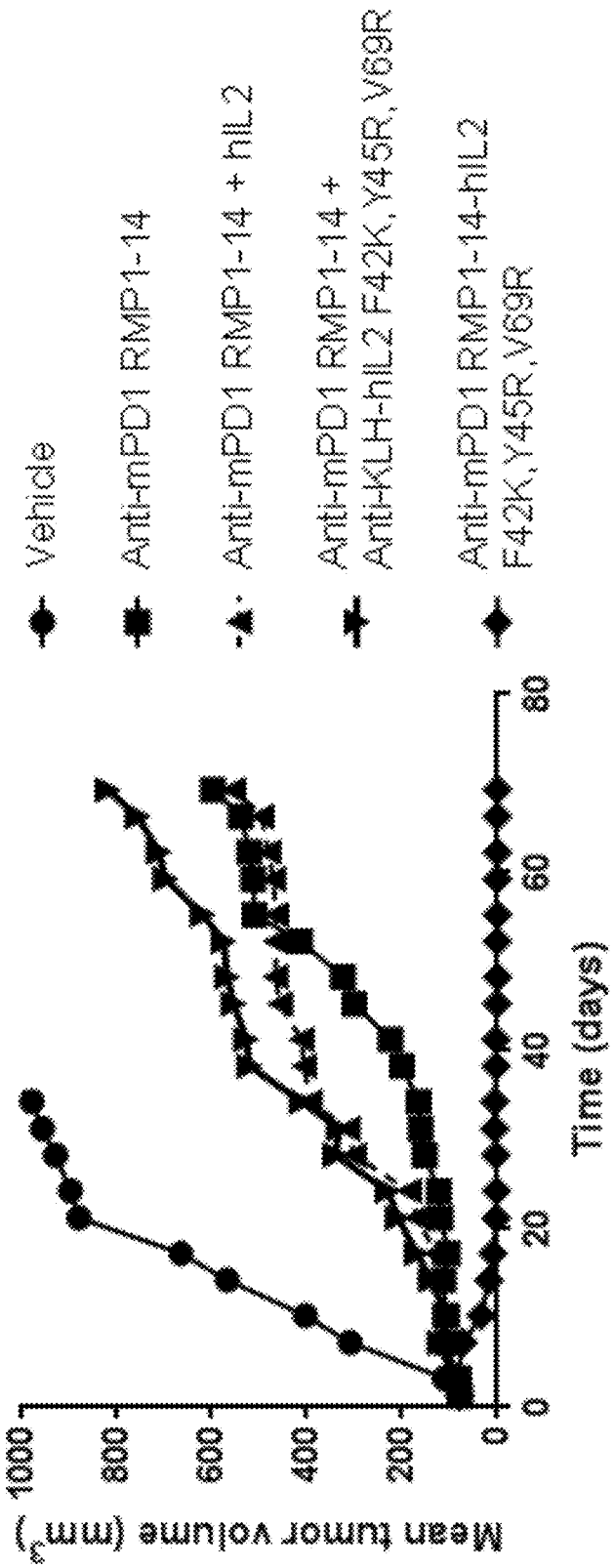

Vehicle
Anti-mPD1 RMP1-14
Anti-mPD1 RMP1-14 + hIL2
Anti-mPD1 RMP1-14 + Anti-KLH-hIL2 F42K,Y45R,V69R
Anti-mPD1 RMP1-14-hIL2 F42K,Y45R,V69R
Mean tumor volume (mm3)
1000
800
600
400
200
0
0
20
40
60
80
Time (days)

FIG. 19

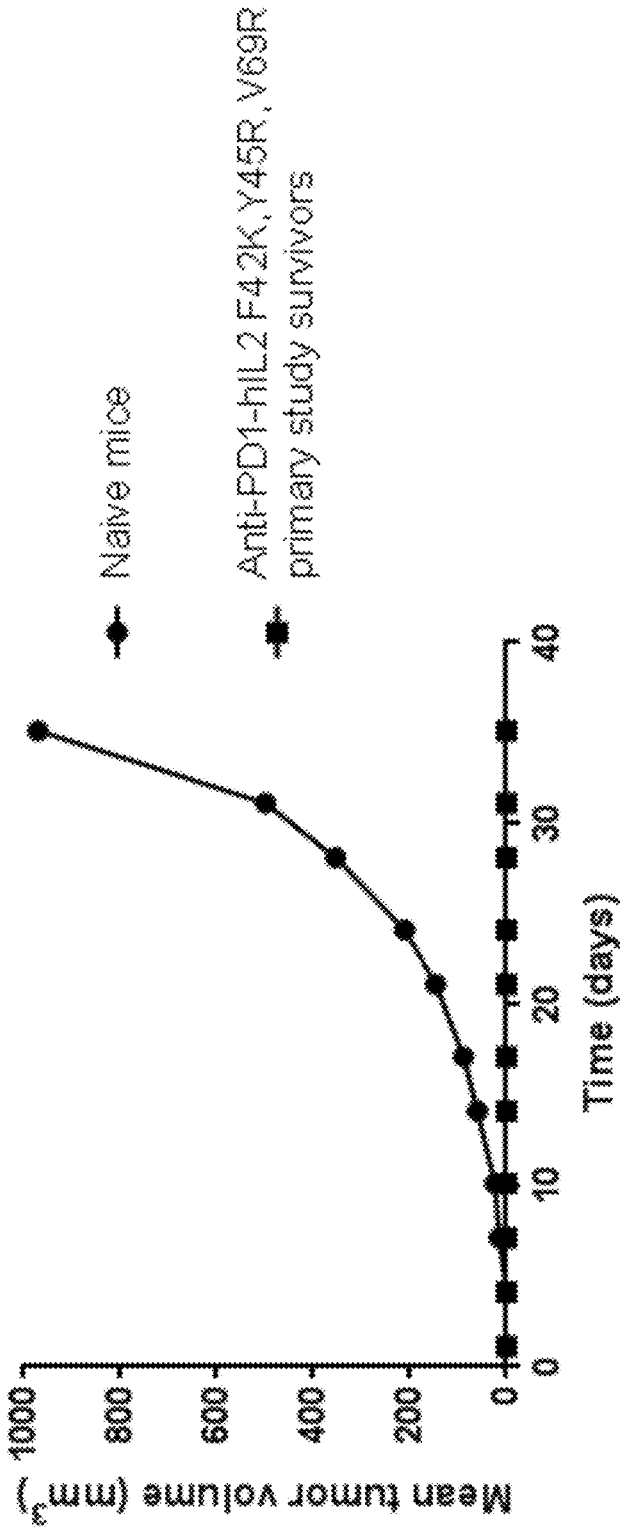

Naive mice
Anti-PD1-hIL2 F42K,Y45R,V69R
primary study survivors
Mean tumor volume (mm³)
1000
800
600
400
200
0
0
10
20
30
40
Time (days)

FIG. 20

ANTI-PD-1 ANTIBODY-ATTENUATED IL-2 IMMUNOCONJUGATES AND USES THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a continuation of U.S. application Ser. No. 18/335,650, which was filed on Jun. 15, 2023, which claims priority to U.S. Provisional Application No. 63/352,842, which was filed on Jun. 16, 2022, U.S. Provisional Application No. 63/481,630, which was filed on Jan. 26, 2023, and U.S. Provisional Application No. 63/502,746, which was filed on May 17, 2023, the disclosure of each of which are hereby incorporated by reference in their entirety.

SEQUENCE LISTING

The instant application contains a Sequence Listing which is being submitted herewith electronically in XML format and is hereby incorporated by reference in its entirety. Said XML copy, created on Aug. 26, 2024, is named 102085.002045_Sequence Listing.xml and is 696,000 bytes in size.

TECHNICAL FIELD

Disclosed herein are modified human interleukin-2 (hIL-2) proteins, human antibody molecules, or antigen-binding fragments thereof, that immunospecifically bind to human programmed cell death protein-1 (hPD-1), and immunoconjugates comprising the same.

BACKGROUND

Human IL-2 (hIL-2) is a Type 1 four α-helical bundle, glycosylated cytokine produced by CD4+ T cells and CD8+ T cells. Autocrine and paracrine IL-2 signaling occurs through engagement of either a high-affinity trimeric receptor complex comprising IL-2Rα (CD25), IL-2Rβ (CD122), and IL-2Rγ (CD132), or an intermediate-affinity dimeric receptor complex which comprises IL-2Rβ (CD122) and IL-2Rγ (CD132). IL-2 has dual opposing and pleiotropic roles, in that it can both stimulate T cell proliferation to generate T cell effector, T cell memory, and activated NK cells, but can also stimulate suppressive regulatory T cells for maintenance of immune homeostasis. Low-dose IL-2 primarily stimulates regulatory T cells as well as some T effector and NK cells, whereas high-dose IL-2 broadly stimulates cytotoxic T cells, T effector, and NK cells and regulatory T cells. The use of IL-2 in the treatment of autoimmune diseases and as a cancer immunotherapy has, however, been limited by off-target effects and toxicity associated with the administration of IL-2.

SUMMARY

Disclosed herein are modified human interleukin-2 (hIL-2) proteins comprising a substitution at amino acid position 20 and a substitution at amino acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345, wherein the modified hIL-2 protein exhibits reduced potency on both a high affinity hIL-2 receptor and on an intermediate affinity hIL-2 receptor relative to the non-modified hIL-2.

Also disclosed herein are modified human interleukin-2 (hIL-2) proteins comprising a D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitution at amino acid position 20 and a R38E substitution at amino acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Also disclosed herein are human antibody molecules, or antigen-binding fragments thereof, that immunospecifically bind to human programmed cell death protein-1 (hPD-1), wherein the human antibody molecule or antigen-binding fragment thereof comprises:

a) a heavy chain complementarity determining region 1 (CDR1) comprising the amino acid sequence of SEQ ID NO: 418, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 419, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 420, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 421, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 422, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 423;

b) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 386, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 387, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 388, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 389, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 390, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 391;

c) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 396, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 397, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 398, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 399, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 400, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 401; or

d) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 406, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 407, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 408, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 409, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 410, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 411.

Also disclosed herein are immunoconjugates comprising:

(a) a modified hIL-2 protein comprising a substitution at amino acid position 20 and a substitution at amino acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345; and

(b) a human antibody molecule, or antigen-binding fragment thereof, that immunospecifically binds to hPD-1, wherein the human antibody molecule or antigen-binding fragment thereof comprises:

(i) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 418, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 419, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 420, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 421, a light chain CDR2 comprising the amino acid

sequence of SEQ ID NO: 422, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 423;

(ii) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 386, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 387, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 388, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 389, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 390, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 391;

(iii) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 396, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 397, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 398, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 399, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 400, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 401; or

(iv) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 406, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 407, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 408, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 409, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 410, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 411.

Pharmaceutical compositions comprising any of the herein disclosed modified hIL-2 proteins, human antibody molecules, or antigen-binding fragments thereof, or immunoconjugates are also disclosed.

Also disclosed herein are polynucleotides comprising a nucleic acid sequence encoding any of the herein disclosed modified hIL-2 proteins, human antibody molecules, or antigen-binding fragments thereof, or immunoconjugates, as well as vectors comprising the polynucleotides and transformed cells comprising the vectors.

Disclosed herein are methods of treating a disease or disorder in a subject, the methods comprising administering a therapeutically effective amount of any of the herein disclosed immunoconjugates or pharmaceutical compositions to the subject to thereby treat the disease or disorder.

Also disclosed are uses of any of the herein disclosed immunoconjugates or pharmaceutical compositions in the preparation of a medicament for the treatment of a disease, and uses of any of the herein disclosed immunoconjugates or pharmaceutical compositions for the treatment of a disease or disorder.

BRIEF DESCRIPTION OF THE DRAWINGS

The summary, as well as the following detailed description, is further understood when read in conjunction with the appended drawings. For the purpose of illustrating the disclosed modified hIL-2 proteins, anti-hPD-1 antibodies or antigen-binding fragments thereof, and immunoconjugates, there are shown in the drawings exemplary embodiments of the modified hIL-2 proteins, anti-hPD-1 antibodies or antigen-binding fragments thereof, and immunoconjugates; however, the modified hIL-2 proteins, anti-hPD-1 antibodies or antigen-binding fragments thereof, and immunoconjugates are not limited to the specific embodiments disclosed. In the drawings:

FIG. **1**A, FIG. **1**B, FIG. **1**C, FIG. **1**D, FIG. **1**E, FIG. **1**F, FIG. **1**G, and FIG. **1**H illustrate exemplary antibody-hIL-2 immunoconjugates as described in Example 1 herein. Non-attenuated human IL-2 cytokine (grey rectangle) was fused either directly (df) or via an L6 linker (L6) to either the N-terminus or C-terminus of both heavy chains or both kappa light chains of the antibody.

FIG. **2**A, FIG. **2**B, FIG. **2**C, FIG. **2**D, FIG. **2**E, FIG. **2**F, FIG. **2**G, and FIG. **2**H illustrate exemplary antibody-hIL-2 immunoconjugates with hCD25 (1-164) extracellular domain designed to interfere with the immunoconjugate's hIL-2 binding to the human IL-2Rα. For N-terminal variants, the human CD25/IL-2Rα extracellular domain (black triangle) was fused to a non-attenuated hIL-2 cytokine (grey rectangle) via an L20 linker (light grey line). Non-attenuated hIL-2 cytokine was then either directly fused (df) or fused to the antibody with an L6 linker. For C-terminal variants, the hCD25/IL-2Rα extracellular domain moiety was either directly fused (df) or fused to the antibody using an L6 linker, followed by an L20 linker and non-attenuated hIL-2 cytokine.

FIG. **3** illustrates an exemplary 1H3-hIgG1-L6-hIL-2 immunoconjugate that contains a CD25/IL-2Rα extracellular domain moiety. The hCD25/IL-2Rα extracellular domain moiety was fused to the 1H3-hIgG1-L6-hIL-2 at the C-terminus of each heavy chain via an L6 linker followed by an L20 linker and hIL-2 cytokine moiety containing substitutions predicted to modulate binding to CD122/IL-2Rβ as described in Example 2 (attenuated hIL-2).

FIG. **4**A, FIG. **4**B, FIG. **4**C, and FIG. **4**D show the results of experiments analyzing the binding of the anti-hPD-1 antibodies 2H7-hIgG4, C51E6-5-hIgG4, and A2-hIgG4 to the human PD-1 receptor on Jurkat cells in the presence of saturating concentrations of anti-hPD-1 #1-mIgG2b-N297A and anti-hPD-1 #2-mIgG2b-N297A (10 μM) prior to exposure with anti-hPD-1 antibodies.

FIG. **5** illustrates exemplary anti-hPD-1-attenuated hIL-2 immunoconjugates either with an L6 linker (L6) (left) or direct fusion (df) (right). Anti-hPD-1 antibodies comprising either hIgG4 or hIgG1 Fc domains, with or without L235E (LE) or L235A/G237A (LAGA) modifications in the Fc domain, were fused to attenuated hIL-2 cytokines at the C-terminus of the antibody heavy chains. Various substitutions in the hIL-2 cytokine were introduced for potency attenuation.

FIG. **6**A and FIG. **6**B show the results of competition assays demonstrating that anti-hPD-1 #1-mIgG2b-N297A (FIG. **6**A) or anti-hPD-1 #2-mIgG2b-N297A (FIG. **6**B) bind to anti-hPD-1 receptor on Jurkat cells in the presence of saturating concentrations of anti-hPD-1-attenuated hIL-2 immunoconjugates (280 nM).

FIG. **7** shows the results of competition assays demonstrating that the anti-hPD-1-attenuated hIL-2 immunoconjugates 2H7-hIgG4-df-hIL-2 (D20A/R38E), C51E6-5-L6-hIgG4-hIL-2 (D20A/R38E), and A2-hIgG4-df-hIL-2 (D20A/R38E) do not inhibit the binding of human PD-L1 to the human PD-1 receptor using the PD-1/PD-L1 Blockade Bioassay.

FIG. **8** shows the results of experiments analyzing the effect of the administration of vehicle, surrogate anti-PD-1 antibodies (anti-mPD-1 RMP1-14 mIgG2b-N297A and anti-mPD-1 RMP1-30 mIgG2b-N297A), and surrogate anti-PD-1-attenuated hIL-2 immunoconjugates (anti-mPD-1 RMP1-14 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) or anti-

mPD-1 RMP1-30 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)) on the growth of established subcutaneous MC38 syngeneic tumors in C57BL/6 mice, as described in Example 18. Test agents were dosed intraperitoneally at 5 mg/kg twice weekly for 4 weeks, starting on day 1. The points on the graph represent mean tumor volumes of an average of 10 mice per group.

FIG. **9**A, FIG. **9**B, and FIG. **9**C illustrate the results of studies conducted to determine the efficacy of surrogate anti-hPD-1-attenuated hIL-2 immunoconjugate anti-mPD-1 RMP1-30 mIgG2b-N297A-hIL-2 (F42K/Y45R/V69R) in an MC38 murine colon adenocarcinoma model. FIG. **9**A depicts the mean subcutaneous tumor volumes (mm^3) measured every 3-4 days for 8 days after the first dose of test agents (3 doses on days 1, 4, and 8 at 5 mg/kg). Tumor growth curves represent an average of 15 animals per group. FIG. **9**B summarizes results from immunophenotyping tumors by flow cytometry on day 9, showing the proportion of different $CD8^+$ T cell subsets as fractions of the total $CD8^+$ T cell average absolute counts. FIG. **9**C illustrates immunophenotyping results on day 9 which demonstrated that there was a significant expansion of $CD8^+$ T effector memory and a trend towards decreased regulatory T cells in tumors (cells/μL) following exposure to the surrogate immunoconjugate.

FIG. **10** shows the results from an experiment analyzing the acceleration of Graft vs Host Disease in NOD-Prkdc^{em26Cd52}IL-2rg^{em26Cd22}/NjuCrl (NCG) mice exposed to anti-hPD-1-attenuated hIL-2 immunoconjugates, as demonstrated by significant body weight decrease in an NCG-PBMC model.

FIG. **11**A and FIG. **11**B show the results of an experiment analyzing the dose-dependent expansion of cells/mL of blood $CD8^+$ Effector Memory T cells (FIG. **11**A) and $CD4^+$ Effector Memory T cells (FIG. **11**B) of NOD-Prkdc^{em26cd2}IL-2rg^{em26Cd22}/NjuCrl (NCG) mice treated with 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) in the NCG-PBMC model.

FIG. **12** shows a decrease in cells/mL of blood regulatory T cells of NOD-Prkdc^{em26Cd52}IL-2rg^{em26Cd22}/NjuCrl (NCG) mice treated with 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) in the NCG-PBMC model.

FIG. **13**A and FIG. **13**B show that H7-632-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) (designated "H7-767") (FIG. **13**B) continues to bind to the human PD-1 receptor on Jurkat cells in the presence of saturating concentrations of anti-hPD-1 #1-mIgG2b-N297A and anti-hPD-1 #2-mIgG2b-N297A (10 μM) prior to exposure.

FIG. **14**A and FIG. **14**B are graphs showing the binding of recombinant human PD-1 captured by H7-767 immobilized to a CM5 sensor chip followed by binding of either (FIG. **14**A) H7-767, KEYTRUDA®, or OPDIVO® or (FIG. **14**B) PD-L1 or PD-L2, as evaluated by surface plasmon resonance (SPR).

FIG. **15** demonstrates that H7-632-hIgG1-LAGA and H7-767 do not inhibit the binding of human PD-L1 to the human PD-1 receptor using an hPD-1/hPD-L1 Blockade Bioassay.

FIG. **16**A, FIG. **16**B, FIG. **16**C, and FIG. **16**D are graphs showing the binding of anti-hPD-1-attenuated hIL-2 immunoconjugates 2H7-hIgG4-df-hIL-2 (D20A/R38E), C51E6-5-hIgG4-df-hIL-2 (D20A/R38E), and A2-hIgG4-df-hIL-2 (D20A/R38E) to the human PD-1 receptor on Jurkat cells in the presence of saturating concentrations of anti-hPD-1 #1-mIgG2b-N297A and anti-hPD-1 #2-mIgG2b-N297A (10 μM) prior to exposure with anti-hPD-1-attenuated hIL-2 immunoconjugates, as assessed by flow cytometry.

FIG. **17** is a graph showing the binding of 2H7-hIgG4-df-hIL-2 (D20A/R38E), C51E6-5-hIgG4-df-hIL-2 (D20A/R38E), A2-hIgG4-df-hIL-2 (D20A/R38E) and the irrelevant antibody control 1H3-hIgG4-df-hIL-2 (D20A/R38E) to HEK-293T cells recombinantly expressing cynomolgus PD-1, as assessed by flow cytometry.

FIG. **18**A, FIG. **18**B, FIG. **18**C, and FIG. **18**D show the antagonist activity of anti-hPD-1-attenuated hIL-2 immunoconjugates 2H7-hIgG4-df-hIL-2 (D20A/R38E), C51E6-5-hIgG4-df-hIL-2 (D20A/R38E), and A2-hIgG4-df-hIL-2 (D20A/R38E) in the presence of anti-hPD-1 #1 or anti-hPD-1 #2. FIG. **18**A and FIG. **18**B show results from the titration of anti-hPD-1 #1 or anti-hPD-1 #2 in the presence of fixed concentration anti-hPD-1-attenuated hIL-2 immunoconjugates. FIG. **18**C and FIG. **18**D show the results from the converse experiment in which anti-hPD-1-attenuated hIL-2 immunoconjugates were titrated with a fixed concentration of 100 nM of anti-hPD-1 #1 (FIG. **18**C) or 100 nM of anti-hPD-1 #2 (FIG. **18**D).

FIG. **19** shows the effect of the administration of various test agents including a surrogate anti-mouse PD-1/attenuated IL-2 immunoconjugate on the growth of established subcutaneous MC38 syngeneic tumors in C57BL/6 mice. Each growth curve represents the mean tumor volume of ten mice per treatment group.

FIG. **20** shows the ability of MC38 tumor cells to grow in tumor naïve mice compared to mice from the MC38 primary tumor study illustrated in FIG. **19** that were previously dosed with anti-mPD-1-hIL-2 F42K/Y45R/V69R and which had demonstrated complete long-term regression of the established primary tumor. Animals from both cohorts (10 mice per group) were subcutaneously implanted with 5×10^5 MC38 tumor cells on the left flank contralateral to the location of the primary tumor. Mice previously exposed to the surrogate agent anti-mPD-1-hIL-2 F42K/Y45R/V69R demonstrated no tumor growth as they had developed a sustained immunity, whilst corresponding naïve mice controls demonstrated the typical growth of tumors in their flanks.

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

The disclosed modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates may be understood more readily by reference to the following detailed description taken in connection with the accompanying figures, which form a part of this disclosure. It is to be understood that the disclosed modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates are not limited to the specific modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates described and/or shown herein, and that the terminology used herein is for the purpose of describing particular embodiments by way of example only and is not intended to be limiting of the claimed modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates.

Unless specifically stated otherwise, any description as to a possible mechanism or mode of action or reason for improvement is meant to be illustrative only, and the disclosed modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates are not to be constrained by the correctness or incorrectness of any such suggested mechanism or mode of action or reason for improvement.

Throughout this text, the descriptions refer to modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates, as well as methods of using the modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates. Where the disclosure describes or claims a feature or embodiment associated with a modified hIL-2 protein, human antibody molecule or antigen-binding fragment thereof, and immunoconjugate, such a feature or embodiment is equally applicable to the methods of using the modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates. Likewise, where the disclosure describes or claims a feature or embodiment associated with a method of using a modified hIL-2 protein, human antibody molecule or antigen-binding fragment thereof, and immunoconjugate, such a feature or embodiment is equally applicable to the modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates.

Where a range of numerical values is recited or established herein, the range includes the endpoints thereof and all the individual integers and fractions within the range, and also includes each of the narrower ranges therein formed by all the various possible combinations of those endpoints and internal integers and fractions to form subgroups of the larger group of values within the stated range to the same extent as if each of those narrower ranges was explicitly recited. Where a range of numerical values is stated herein as being greater than a stated value, the range is nevertheless finite and is bounded on its upper end by a value that is operable within the context of the herein disclosure. Where a range of numerical values is stated herein as being less than a stated value, the range is nevertheless bounded on its lower end by a non-zero value. It is not intended that the scope of the modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates be limited to the specific values recited when defining a range. All ranges are inclusive and combinable.

When values are expressed as approximations, by use of the antecedent "about," it will be understood that the particular value forms another embodiment. Reference to a particular numerical value includes at least that particular value, unless the context clearly dictates otherwise. The term "about" when used in reference to numerical ranges, cutoffs, or specific values is used to indicate that the recited values may vary by up to as much as 10% from the listed value. Thus, the term "about" is used to encompass variations of +10% or less, variations of +5% or less, variations of +1% or less, variations of +0.5% or less, or variations of +0.1% or less from the specified value.

It is to be appreciated that certain features of the disclosed modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates which are, for clarity, described herein in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the disclosed modified hIL-2 proteins, human antibody molecules or antigen-binding fragments thereof, and immunoconjugates that are, for brevity, described in the context of a single embodiment, may also be provided separately or in any subcombination.

As used herein, the singular forms "a," "an," and "the" include the plural.

Various terms relating to aspects of the description are used throughout the specification and claims. Such terms are to be given their ordinary meaning in the art unless otherwise indicated. Other specifically defined terms are to be construed in a manner consistent with the definitions provided herein.

The term "comprising" is intended to include examples encompassed by the terms "consisting essentially of" and "consisting of"; similarly, the term "consisting essentially of" is intended to include examples encompassed by the term "consisting of."

The term "antibody molecule" is meant in a broad sense and includes full length immunoglobulin molecules and antigen-binding fragments thereof.

Immunoglobulins can be assigned to five major classes, namely IgA, IgD, IgE, IgG, and IgM, depending on the heavy chain constant domain amino acid sequence. IgA and IgG are further sub-classified as the isotypes IgA1, IgA2, IgG1, IgG2, IgG3, and IgG4. Antibody light chains of any vertebrate species can be assigned to one of two clearly distinct types, namely kappa (κ) and lambda (2), based on the amino acid sequences of their constant domains.

"Antigen-binding fragment" refers to a portion of an immunoglobulin molecule that retains the antigen binding properties of the parental full length antibody (i.e., "antigen-binding fragment thereof"). Exemplary antigen binding fragments can have: heavy chain complementarity determining regions (CDR) 1, 2, and/or 3; light chain CDR1, 2, and/or 3; a heavy chain variable region (VH); a light chain variable region (VL); and combinations thereof. Antigen binding fragments include: a Fab fragment, a monovalent fragment consisting of the VL, VH, constant light (CL), and constant heavy 1 (CH1) domains; a F (ab) 2 fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; a Fd fragment consisting of the VH and CH1 domains; a Fv fragment consisting of the VL and VH domains of a single arm of an antibody; and a domain antibody (dAb) fragment (Ward et al., Nature 341:544-546, 1989), which consists of a VH domain or a VL domain. VH and VL domains can be engineered and linked together via a synthetic linker to form various types of single chain antibody designs where the VH/VL domains pair intramolecularly, or intermolecularly in those cases when the VH and VL domains are expressed by separate single chain antibody constructs, to form a monovalent antigen binding site, such as single chain Fv (scFv) or diabody, described for example in Int'l Pat. Pub. Nos. WO1998/44001, WO1988/01649, WO1994/13804, and WO1992/01047. These antibody fragments are obtained using techniques well known to those of skill in the art, and the fragments are screened for utility in the same manner as are full length antibodies.

The phrase "immunospecifically binds" refers to the ability of the disclosed antibody molecules to preferentially bind to its target (hPD-1 in the case of anti-hPD-1 antibody molecules) without preferentially binding other molecules in a sample containing a mixed population of molecules. Antibody molecules that immunospecifically bind hPD-1 are substantially free of other antibodies having different antigenic specificities (e.g., an anti-hPD-1 antibody is substantially free of antibodies that specifically bind antigens other than hPD-1). Antibody molecules that immunospecifically bind hPD-1, however, can have cross-reactivity to other antigens, such as orthologs of hPD-1, including *Macaca fascicularis* (cynomolgus monkey) PD-1. The antibody molecules disclosed herein are able to immunospecifically bind both naturally-produced hPD-1 and to PD-1 which is recombinantly produced in mammalian or prokaryotic cells.

An antibody variable region consists of four "framework" regions interrupted by three "antigen binding sites." The antigen binding sites are defined using various terms: (i) Complementarity Determining Regions (CDRs), three in the VH (HCDR1, HCDR2, HCDR3), and three in the VL (LCDR1, LCDR2, LCDR3) are based on sequence variability (Wu and Kabat J Exp Med 132:211-50, 1970; Kabat et al., Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md., 1991); and (ii) "Hypervariable regions" ("HVR" or "HV"), three in the VH (H1, H2, H3) and three in the VL (L1, L2, L3) refer to the regions of the antibody variable domains which are hypervariable in structure as defined by Chothia and Lesk (Chothia and Lesk Mol Biol 196:901-17, 1987). The AbM definition of CDRs is also widely used; it is a compromise between Kabat and Chothia numbering schemes and is so-called because it was used by Oxford Molecular's AbM antibody modelling software (Rees, A. R., Searle, S. M. J., Henry, A. H. and Pedersen, J. T. (1996) In Sternberg M. J. E. (ed.), Protein Structure Prediction. Oxford University Press, Oxford, 141-172). Other terms include "IMGT-CDRs" (Lefranc et al., Dev Comparat Immunol 27:55-77, 2003) and "Specificity Determining Residue Usage" (SDRU) (Almagro Mol Recognit 17:132-43, 2004). The International ImMunoGeneTics (IMGT) database (http://www_imgt_org) provides a standardized numbering and definition of antigen-binding sites. The correspondence between CDRs, HVs and IMGT delineations is described in Lefranc et al., Dev Comparat Immunol 27:55-77, 2003.

"Framework" or "framework sequences" are the remaining sequences of a variable region other than those defined to be antigen binding sites. Because the antigen binding sites can be defined by various terms as described above, the exact amino acid sequence of a framework depends on how the antigen-binding site was defined.

"Human antibody," "fully human antibody," and like terms refers to an antibody having heavy and light chain variable regions in which both the framework and the antigen binding sites are derived from sequences of human origin. If the antibody contains a constant region, the constant region also is derived from sequences of human origin. A human antibody comprises heavy and/or light chain variable regions that are "derived from" sequences of human origin if the variable regions of the antibody are obtained from a system that uses human germline immunoglobulin or rearranged immunoglobulin genes. Such systems include human immunoglobulin gene libraries displayed on phage, and transgenic non-human animals such as mice or chicken carrying human immunoglobulin loci as described herein. "Human antibody" may contain amino acid differences when compared to the human germline or rearranged immunoglobulin sequences due to, for example, naturally occurring somatic mutations or intentional introduction of substitutions in the variable domain (framework and antigen binding sites), or constant domain. Typically, a "human antibody" is at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical in amino acid sequence to an amino acid sequence encoded by a human germline or rearranged immunoglobulin gene. In some cases, a "human antibody" may contain consensus framework sequences derived from human framework sequence analyses, for example as described in Knappik et al., J Mol Biol 296:57-86, 2000, or synthetic HCDR3 incorporated into human immunoglobulin gene libraries displayed on phage, as described in, for example, Shi et al., J Mol Biol 397:385-96, 2010 and Int'l Pat. Pub. No. WO2009/085462. Antibodies in which antigen binding sites are derived from a non-human species are not included in the definition of "human antibody."

Human antibodies, while derived from human immunoglobulin sequences, may be generated using systems such as phage display incorporating synthetic CDRs and/or synthetic frameworks, or can be subjected to in vitro mutagenesis to improve antibody properties in the variable regions or the constant regions or both, resulting in antibodies that do not naturally exist within the human antibody germline repertoire in vivo.

"Recombinant antibody" includes all antibodies that are prepared, expressed, created, or isolated by recombinant means, such as: antibodies isolated from an animal (e.g., a mouse) that is transgenic or transchromosomal for human immunoglobulin genes or a hybridoma prepared therefrom (described further below); antibodies isolated from a host cell transformed to express the antibody; antibodies isolated from a recombinant, combinatorial antibody library; and antibodies prepared, expressed, created, or isolated by any other means that involve splicing of human immunoglobulin gene sequences to other DNA sequences, or antibodies that are generated in vitro using Fab arm exchange.

"Monoclonal antibody" refers to a population of antibody molecules of a single molecular composition. A monoclonal antibody composition displays a single binding specificity and affinity for a particular epitope, or in a case of a bispecific monoclonal antibody, a dual binding specificity to two distinct epitopes. Monoclonal antibody therefore refers to an antibody population with single amino acid composition in each heavy and each light chain, except for possible well known alterations such as removal of C-terminal lysine from the antibody heavy chain. Monoclonal antibodies may have heterogeneous glycosylation within the antibody population. Monoclonal antibody may be monospecific or multispecific, or monovalent, bivalent or multivalent. A bispecific antibody is included in the term monoclonal antibody.

"Epitope" refers to a portion of an antigen to which an antibody specifically binds. Epitopes usually consist of chemically active (such as polar, non-polar, or hydrophobic) surface groupings of moieties such as amino acids or polysaccharide side chains and can have specific three-dimensional structural characteristics, as well as specific charge characteristics. An epitope can be composed of contiguous and/or discontiguous amino acids that form a conformational spatial unit. For a discontiguous epitope, amino acids from differing portions of the linear sequence of the antigen come in close proximity in 3-dimensional space through the folding of the protein molecule.

"Variant" refers to a polypeptide or a polynucleotide that differs from a reference polypeptide or a reference polynucleotide by one or more modifications for example, substitutions, insertions, or deletions. The term "mutation" as used herein is intended to mean one or more intentional substitutions which are made to a polypeptide or polynucleotide.

"Treat," "treatment," and like terms refer to both therapeutic treatment and prophylactic or preventative measures, and includes reducing the severity and/or frequency of symptoms, eliminating symptoms and/or the underlying cause of the symptoms, reducing the frequency or likelihood of symptoms and/or their underlying cause, and improving or remediating damage caused, directly or indirectly, by the disease or disorder. Treatment also includes prolonging survival as compared to the expected survival of a subject not receiving treatment. Subjects to be treated include those

that have the disease or disorder as well as those prone to have the disease or disorder or those in which the disease or disorder is to be prevented.

As used herein, "administering to the subject" and similar terms indicate a procedure by which the disclosed modified hIL-2 proteins, immunoconjugates, or pharmaceutical compositions are injected into a subject such that target cells, tissues, or segments of the body of the subject are contacted with the disclosed modified hIL-2 proteins or immunoconjugates comprising the same.

The phrase "therapeutically effective amount" refers to an amount of the modified hIL-2 proteins, immunoconjugates, or pharmaceutical compositions, as described herein, effective to achieve a particular biological or therapeutic result such as, but not limited to, biological or therapeutic results disclosed, described, or exemplified herein. The therapeutically effective amount may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the modified hIL-2 proteins, immunoconjugates, or pharmaceutical compositions to cause a desired response in a subject. Exemplary indicators of a therapeutically effect amount include, for example, improved well-being of the patient, reduction of a disease symptom, arrested or slowed progression of disease symptoms, and/or absence of disease symptoms.

The term "subject" as used herein is intended to mean any animal, in particular, mammals. Thus, the methods are applicable to human and nonhuman animals, although most preferably used with humans. "Subject" and "patient" are used interchangeably herein.

Immunoconjugate and fusion protein are used interchangeably herein.

Modified Human Interleukin-2 (hIL-2) Proteins

Disclosed herein are modified hIL-2 proteins comprising a substitution at amino acid position 20 and a substitution at amino acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345, wherein the modified hIL-2 protein exhibits reduced potency on both a high affinity hIL-2 receptor and on an intermediate affinity hIL-2 receptor relative to a non-modified hIL-2. The disclosed modified hIL-2 proteins are also referred to as "attenuated" hIL-2 herein.

Suitable substitutions at amino acid position 20 include, for example, any one of a D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitution.

Suitable substitutions at amino acid position 38 include, for example, any one of an R38E, R38N, R38G, R38H, R38I, R38L, R38M, R38F, R38P, R38S, R38T, R38W, R38Y, R38V, R38A, R38Q, R38D, or an R38K substitution.

In some embodiments, any one of the D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitutions can be combined with an R38E substitution.

The modified hIL-2 proteins can comprise the amino acid sequence of any one of SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620. The modified hIL-2 proteins can comprise the amino acid sequence of any one of SEQ ID NOs: 134-150, 307, 344, 608, 611, 614, or 620. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 134. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 135. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 136. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 137. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 138. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 139. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 140. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 141. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 142. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 143. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 144. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 145. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 146. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 147. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 148. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 149. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 150. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 307. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 344. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 607. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 608. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 609. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 610. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 611. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 614. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 617. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 620. The modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 can further comprise a T3A substitution and/or a C125A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 further comprises a T3A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 further comprises a C125A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 further comprises a T3A substitution and a C125A substitution.

The modified hIL-2 proteins may comprise a D20A substitution and a R38E substitution.

As described herein the term "reduced potency" and related terms such as "reduction in potency" or "attenuation" of IL-2 activity refer to a reduction in potency of the modified hIL-2 as determined by an increased EC_{50} value relative to the EC_{50} value for an non-modified-hIL-2 in an IL-2-dependent assay. As described herein the reduction in potency of the modified hIL-2 will be on both the high affinity and on the intermediate affinity IL-2 receptors. The IL-2-dependent assay for determining potency may be an engineered human erythroleukemic TF1 (TF1+IL-2RB) or a human natural killer NK-92 cell proliferation assay as described herein. In one embodiment, the IL-2-dependent

assay for determining potency is an engineered human erythroleukemic TF1 (TF1+IL-2RB) cell proliferation assay. In another embodiment, the IL-2-dependent assay for determining potency is a human natural killer NK-92 cell proliferation assay. Other IL-2-dependent assays for determining potency may also be a TF1+IL-2Rβ or a human natural killer NK-92 pSTAT5 assay as described herein. The non-modified-hIL-2 may be a prokaryote-expressed hIL-2 such as Proleukin® (which has the native human IL-2 amino acid sequence apart from a C125S substitution to remove an unbound cysteine, and which does not bear the normal human carbohydrate expression on residue T3), or the non-modified-hIL-2 may be an hIL-2 with the amino acid sequence of SEQ ID NO: 345 or with the amino acid sequence of SEQ ID NO: 345 with a C125S substitution, which is expressed in a mammalian cell line, such as a CHO or HEK cell line.

The modified hIL-2 proteins can further comprise a substitution at amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. A suitable substitution includes, for example, a T3A. In some embodiments, the modified hIL-2 proteins comprise a T3A substitution, a D20A substitution, and a R38E substitution. In some aspects, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 216.

Alternatively, the modified hIL-2 proteins can further comprise a deletion of amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. In some embodiments, the modified hIL-2 proteins comprise a deletion of amino acids 1-3, a D20A substitution, and a R38E substitution. In some aspects, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 218.

The modified hIL-2 proteins can further comprise a deletion or substitution at amino acid position 125 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. The substitution at amino acid position 125 can be C125A. In some embodiments, the modified hIL-2 proteins comprise a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 215. In some embodiments, the modified hIL-2 proteins comprise a T3A substitution, a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 217. In some embodiments, the modified hIL-2 proteins comprise a deletion of amino acids 1-3, a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 219.

The modified hIL-2 proteins can exhibit a reduction in potency of at least about 200-fold, at least about 500-fold, at least about 1,000-fold, at least about 2,000-fold, at least about 5,000-fold, at least about 6,500-fold, or at least about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) relative to a non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. In some embodiments, the modified hIL-2 proteins can exhibit a reduction in potency of greater than about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) relative to a non-modified hIL-2. A greater reduction in hIL-2 potency on the high affinity hIL-2 receptor may be possible and acceptable for the modified hIL-2 proteins described herein, but such a reduction may not be quantifiable with the methods described herein due to limits of the cell proliferation assay conditions.

In addition, the modified hIL-2 proteins can exhibit a reduction in potency of at least about 200-fold, at least about 500-fold, at least about 1,000-fold, at least about 2,000-fold, at least about 5,000-fold, at least about 6,500-fold, or at least about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to an non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. In some embodiments, the modified hIL-2 proteins can exhibit a reduction in potency of greater than about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2.

The modified hIL-2 proteins can exhibit a reduction in potency of up to about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) and a reduction in potency of up to about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. The modified hIL-2 proteins can exhibit a reduction in potency of greater than about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) and a reduction in potency of greater than about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2

As demonstrated herein, the modified hIL-2 proteins can be fused to an anti-PD-1 antibody or an antigen-binding fragment thereof. The hIL-2 proteins can fused to the anti-PD-1 antibody or an antigen-binding fragment thereof at the N-terminus of an antibody light chain, the C-terminus of an antibody light chain, the N-terminus of an antibody heavy chain, the C-terminus of an antibody heavy chain, the N-terminus of the antigen-binding fragment, or the C-terminus of the antigen-binding fragment. In some embodiments, the modified hIL-2 protein is directly fused by a peptide bond to the anti-PD-1 antibody or an antigen-binding fragment thereof. The modified hIL-2 proteins can be, for example, directly fused by a peptide bond to the C-terminal amino acid residue of the anti-PD-1 antibody heavy chain. In some embodiments, the modified hIL-2 protein is fused to the anti-PD-1 antibody or an antigen-binding fragment thereof through a linker.

Fusion of the modified hIL-2 proteins to the antibody or antigen-binding fragments thereof can rescue the modified hIL-2 proteins' ability to bind to and activate the human intermediate affinity IL-2 receptor on PD-1-expressing cells such as T cells and in particular tumor-infiltrating lymphocytes. In some embodiments, the hIL-2 protein that is fused to the antibody or an antigen-binding fragment thereof exhibits potency on the intermediate affinity IL-2 receptor on PD-1-expressing cells that is comparable to the potency of wild type hIL-2 on the intermediate affinity IL-2 receptor.

Fusion of the modified hIL-2 protein to an antibody or antigen-binding fragment thereof can be used to selectively deliver IL-2 signaling to cells expressing the PD-1 target of the antibody or antigen-binding fragment thereof. Without being bound by theory, it is believed that targeting the modified hIL-2 protein to specific cell populations can dramatically amplify the therapeutic effects of the IL-2 (e.g., anti-tumor immunity) without off-target systemic toxicities.

Also disclosed herein are modified human interleukin-2 (hIL-2) proteins comprising a D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitution at amino acid position 20 and a R38E substitution at amino

acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

The modified hIL-2 proteins can comprise the amino acid sequence of any one of SEQ ID NOs: 307, 607-611, 614, 617, or 620. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 307. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 607. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 608. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 609. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 610. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 611. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 614. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 617. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 620. The modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 307, 607-611, 614, 617, or 620 can further comprise a T3A substitution and/or a C125A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 307, 607-611, 614, 617, or 620 further comprises a T3A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 307, 607-611, 614, 617, or 620 further comprises a C125A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 307, 607-611, 614, 617, or 620 further comprises a T3A substitution and a C125A substitution.

The modified hIL-2 proteins may comprise a D20A substitution and a R38E substitution. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 149.

The modified hIL-2 proteins can further comprise a substitution at amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. A suitable substitution includes, for example, a T3A. In some embodiments, the modified hIL-2 proteins comprise a T3A substitution, a D20A substitution, and a R38E substitution. In some aspects, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 216.

Alternatively, the modified hIL-2 proteins can further comprise a deletion of amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. In some embodiments, the modified hIL-2 proteins comprise a deletion of amino acids 1-3, a D20A substitution, and a R38E substitution. In some aspects, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 218.

The modified hIL-2 proteins can further comprise a deletion or substitution at amino acid position 125 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. The substitution at amino acid position 125 can be C125A. In some embodiments, the modified hIL-2 proteins comprise a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 215. In some embodiments, the modified hIL-2 proteins comprise a T3A substitution, a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 217. In some embodiments, the modified hIL-2 proteins comprise a deletion of amino acids 1-3, a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 219.

The modified hIL-2 proteins can exhibit a reduction in potency of at least about 200-fold, at least about 500-fold, at least about 1,000-fold, at least about 2,000-fold, at least about 5,000-fold, at least about 6,500-fold, or at least about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) relative to a non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. In some embodiments, the modified hIL-2 proteins can exhibit a reduction in potency of greater than about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) relative to a non-modified hIL-2. A greater reduction in hIL-2 potency on the high affinity hIL-2 receptor may be possible and acceptable for the modified hIL-2 proteins described herein, but such a reduction may not be quantifiable with the methods described herein due to limits of the cell proliferation assay conditions.

In addition, the modified hIL-2 proteins can exhibit a reduction in potency of at least about 200-fold, at least about 500-fold, at least about 1,000-fold, at least about 2,000-fold, at least about 5,000-fold, at least about 6,500-fold, or at least about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to an non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. In some embodiments, the modified hIL-2 proteins can exhibit a reduction in potency of greater than about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2.

The modified hIL-2 proteins can exhibit a reduction in potency of up to about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rβγ) and a reduction in potency of up to about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. The modified hIL-2 proteins can exhibit a reduction in potency of greater than about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) and a reduction in potency of greater than about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2.

As demonstrated herein, the modified hIL-2 proteins can be fused to an anti-PD-1 antibody or an antigen-binding fragment thereof. The hIL-2 proteins can fused to the anti-PD-1 antibody or an antigen-binding fragment thereof at the N-terminus of an antibody light chain, the C-terminus of an antibody light chain, the N-terminus of an antibody heavy chain, the C-terminus of an antibody heavy chain, the N-terminus of the antigen-binding fragment, or the C-terminus of the antigen-binding fragment. In some embodiments, the modified hIL-2 protein is directly fused by a peptide bond to the anti-PD-1 antibody or an antigen-binding fragment thereof. The modified hIL-2 proteins can be, for example, directly fused by a peptide bond to the C-terminal amino acid residue of the anti-PD-1 antibody heavy chain. In some embodiments, the modified hIL-2 protein is fused to the anti-PD-1 antibody or an antigen-binding fragment thereof through a linker.

Fusion of the modified hIL-2 proteins to the antibody or antigen-binding fragments thereof can rescue the modified hIL-2 proteins' ability to bind to and activate the human intermediate affinity IL-2 receptor on PD-1-expressing cells

such as T cells and in particular tumor-infiltrating lymphocytes. In some embodiments, the hIL-2 protein that is fused to the antibody or an antigen-binding fragment thereof exhibits potency on the intermediate affinity IL-2 receptor on PD-1-expressing cells that is comparable to the potency of wild type hIL-2 on the intermediate affinity IL-2 receptor.

Fusion of the modified hIL-2 protein to an antibody or antigen-binding fragment thereof can be used to selectively deliver IL-2 signaling to cells expressing the PD-1 target of the antibody or antigen-binding fragment thereof. Without being bound by theory, it is believed that targeting the modified hIL-2 protein to specific cell populations can dramatically amplify the therapeutic effects of the IL-2 (e.g., anti-tumor immunity) without off-target systemic toxicities.

Human Anti-Human Programmed Cell Death Protein-1 (hPD-1) Antibodies

Disclosed herein are human antibody molecules, or antigen-binding fragments thereof, that immunospecifically bind to hPD-1, wherein the human antibody molecule or antigen-binding fragment thereof comprises:

a) a heavy chain complementarity determining region 1 (CDR1) comprising the amino acid sequence of SEQ ID NO: 418, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 419, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 420, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 421, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 422, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 423;

b) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 386, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 387, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 388, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 389, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 390, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 391;

c) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 396, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 397, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 398, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 399, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 400, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 401; or

d) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 406, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 407, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 408, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 409, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 410, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 411.

In some embodiments, the human antibody molecules, or antigen-binding fragments thereof, comprise a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 418, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 419, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 420, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 421, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 422, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 423 (referred to herein as "H7-632").

In some embodiments, the human antibody molecules, or antigen-binding fragments thereof, comprise a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 386, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 387, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 388, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 389, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 390, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 391 (referred to herein as "2H7").

In some embodiments, the human antibody molecules, or antigen-binding fragments thereof, comprise a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 396, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 397, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 398, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 399, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 400, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 401 (referred to herein as "C51E6-5").

In some embodiments, the human antibody molecules, or antigen-binding fragments thereof, comprise a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 406, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 407, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 408, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 409, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 410, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 411 (referred to herein as "A2").

The disclosed human antibody molecules or antigen-binding fragments thereof, can exhibit one or more of the following activities:

Bind to PD-1 without inhibiting PD-L1 binding to PD-1;

Bind to PD-1 in the presence of standard-of-care anti-PD-1 antibodies used in the clinic (e.g., KEYTRUDAX and OPDIVOX);

Be highly selective for PD-1 and do not immunospecifically bind other related B7 family members; and

Bind to PD-1 on activated human T cells (EC_{50}~0.1-0.2 nM in a flow cytometry binding assay).

The human antibody molecules, or antigen-binding fragments thereof, can comprise a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 416 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 417 (referred to herein as "H7-632").

The human antibody molecules, or antigen-binding fragments thereof, can comprise a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 384 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 385 (referred to herein as "2H7").

The human antibody molecules, or antigen-binding fragments thereof, can comprise a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 394 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 395 (referred to herein as "C51E6-5").

The human antibody molecules, or antigen-binding fragments thereof, can comprise a heavy chain variable region

comprising the amino acid sequence of SEQ ID NO: 404 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 405 (referred to herein as "A2").

The human antibody molecules, or antigen-binding fragments thereof, can comprise a human IgG1 heavy chain constant region.

The human antibody molecules, or antigen binding fragments thereof, can have substitutions or deletions within the constant region to minimize Fc-mediated immune effector function, such as FcγRIIIA-mediated antibody-dependent cell-mediated cytotoxicity (ADCC), FcγRI- and FcγRIIa-dependent antibody-dependent cellular phagocytosis (ADCP), and Clq binding-mediated complement-dependent cytotoxicity (CDC). In some embodiments, the human antibody molecules comprise a L235A substitution, wherein the amino acid numbering is according to EU numbering. In some embodiments, the human antibody molecules comprise a G237A substitution, wherein the amino acid numbering is according to EU numbering. In some embodiments, the human antibody molecules comprise an L235A and a G237A substitution, wherein the amino acid numbering is according to EU numbering.

The human antibody molecules, or antigen-binding fragments thereof, can comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 414 and a light chain comprising the amino acid sequence of SEQ ID NO: 415 (referred to herein as "H7-632-hIgG1-LAGA").

The human antibody molecules, or antigen-binding fragments thereof, can comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 424 and a light chain comprising the amino acid sequence of SEQ ID NO: 425 (referred to herein as "2H7-hIgG4").

The human antibody molecules, or antigen-binding fragments thereof, can comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 426 and a light chain comprising the amino acid sequence of SEQ ID NO: 427 (referred to herein as "C51E6-5-hIgG4").

The human antibody molecules, or antigen-binding fragments thereof, can comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 428 and a light chain comprising the amino acid sequence of SEQ ID NO: 429 (referred to herein as "A2-hIgG4").

The human antibody molecules, or antigen-binding fragments thereof, can be fused to a modified hIL-2 protein comprising a substitution at amino acid position 20 and a substitution at amino acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. The human antibody molecule, or antigen-binding fragments thereof, can be fused to any of the herein disclosed modified hIL-2 proteins.

When not fused to the antibody molecule or antigen-binding fragment thereof, the modified hIL-2 protein can exhibit reduced potency on both a high affinity hIL-2 receptor and on an intermediate affinity hIL-2 receptor relative to a non-modified hIL-2.

Suitable substitutions at amino acid position 20 of the modified hIL-2 include, for example, any one of a D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitution.

Suitable substitutions at amino acid position 38 of the modified hIL-2 protein include, for example, any one of an R38E, R38N, R38G, R38H, R38I, R38L, R38M, R38F, R38P, R38S, R38T, R38W, R38Y, R38V, R38A, R38Q, R38D, or a R38K substitution.

In some embodiments, any one of the D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitutions can be combined with an R38E substitution.

The modified hIL-2 proteins can comprise the amino acid sequence of any one of SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620. The modified hIL-2 proteins can comprise the amino acid sequence of any one of SEQ ID NOs: 134-150, 307, 344, 608, 611, 614, or 620. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 134. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 135. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 136. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 137. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 138. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 139. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 140. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 141. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 142. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 143. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 144. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 145. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 146. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 147. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 148. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 149. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 150. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 307. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 344. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 607. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 608. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 609. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 610. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 611. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 614. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 617. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 620. The modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 can further comprise a T3A substitution and/or a C125A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 further comprises a T3A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 further comprises a C125A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs:

134-150, 307, 344, 607-611, 614, 617, or 620 further comprises a T3A substitution and a C125A substitution.

The modified hIL-2 protein can comprise a D20A substitution and a R38E substitution.

The modified hIL-2 protein can further comprise a substitution at amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. A suitable substitution includes, for example, a T3A. In some embodiments, the modified hIL-2 protein comprises a T3A substitution, a D20A substitution, and a R38E substitution. In some aspects, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 216.

Alternatively, the modified hIL-2 protein can further comprise a deletion of amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. In some embodiments, the modified hIL-2 protein comprises a deletion of amino acids 1-3, a D20A substitution, and a R38E substitution. In some aspects, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 218.

The modified hIL-2 protein can further comprise a deletion or substitution at amino acid position 125 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. The substitution at amino acid position 125 can be C125A. In some embodiments, the modified hIL-2 protein comprises a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 215. In some embodiments, the modified hIL-2 protein comprises a T3A substitution, a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 217. In some embodiments, the modified hIL-2 protein comprises a deletion of amino acids 1-3, a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 219.

When not fused to the human antibody molecules or antigen-binding fragments thereof, the modified hIL-2 proteins can exhibit a reduction in potency of at least about 200-fold, at least about 500-fold, at least about 1,000-fold, at least about 2,000-fold, at least about 5,000-fold, at least about 6,500-fold, or at least about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) relative to a non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. In some embodiments, when not fused to the human antibody molecules or antigen-binding fragments thereof, the modified hIL-2 proteins can exhibit a reduction in potency of greater than about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) relative to a non-modified hIL-2. A greater reduction in hIL-2 potency on the high affinity hIL-2 receptor may be possible and acceptable for the modified hIL-2 proteins described herein, but such a reduction may not be quantifiable with the methods described herein due to limits of the cell proliferation assay conditions.

In addition, when not fused to the human antibody molecules or antigen-binding fragments thereof, the modified hIL-2 proteins can exhibit a reduction in potency of at least about 200-fold, at least about 500-fold, at least about 1,000-fold, at least about 2,000-fold, at least about 5,000-fold, at least about 6,500-fold, or at least about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to an non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. In some embodiments, when not fused to the human antibody molecules or antigen-binding fragments thereof, the modified hIL-2 proteins can exhibit a reduction in potency of greater than about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to an non-modified hIL-2.

When not fused to the human antibody molecules or antigen-binding fragments thereof, the modified hIL-2 proteins can exhibit a reduction in potency of up to about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) and a reduction in potency of up to about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. When not fused to the human antibody molecules or antigen-binding fragments thereof, the modified hIL-2 proteins can exhibit a reduction in potency of greater than about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) and a reduction in potency of greater than about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2.

Fusion of the modified hIL-2 proteins to the antibody or antigen-binding fragments thereof can rescue the modified hIL-2 proteins' ability to bind to and activate the human intermediate affinity IL-2 receptor on PD-1-expressing cells such as T cells and in particular tumor-infiltrating lymphocytes. In some embodiments, the hIL-2 protein that is fused to the antibody or an antigen-binding fragment thereof exhibits potency on the intermediate affinity IL-2 receptor on PD-1-expressing cells that is comparable to the potency of wild type hIL-2 on the intermediate affinity IL-2 receptor

The modified hIL-2 proteins can be fused to the human antibody molecules or antigen-binding fragments thereof at the N-terminus of an antibody light chain, the C-terminus of an antibody light chain, the N-terminus of an antibody heavy chain, the C-terminus of an antibody heavy chain, the N-terminus of the antigen-binding fragment, or the C-terminus of the antigen-binding fragment. In some embodiments, the hIL-2 protein is directly fused by a peptide bond to the antibody or an antigen-binding fragment thereof. The hIL-2 can be, for example, directly fused by a peptide bond to the C-terminal amino acid residue of the antibody heavy chain. In some embodiments, the hIL-2 protein is fused to the antibody or an antigen-binding fragment thereof through a linker.

Fusion of the human antibody molecules or antigen-binding fragments thereof to the modified hIL-2 proteins can be used to selectively deliver IL-2 signaling to cells expressing PD-1. Without being bound by theory, it is believed that targeting the modified hIL-2 protein to specific cell populations expressing PD-1 can dramatically amplify the therapeutic effects of the IL-2 (e.g., anti-tumor immunity) while reducing or minimizing off-target systemic toxicities.

Immunoconjugates

Disclosed herein are immunoconjugates comprising any of the herein disclosed modified hIL-2 proteins and any of the herein disclosed human antibody molecules, or antigen-binding fragments thereof. The immunoconjugates can comprise:

(a) a modified hIL-2 protein comprising a substitution at amino acid position 20 and a substitution at amino acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345; and

(b) a human antibody molecule, or antigen-binding fragment thereof, that immunospecifically binds to hPD-1,

wherein the human antibody molecule or antigen-binding fragment thereof comprises:

(i) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 418, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 419, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 420, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 421, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 422, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 423;

(ii) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 386, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 387, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 388, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 389, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 390, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 391;

(iii) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 396, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 397, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 398, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 399, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 400, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 401; or

(iv) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 406, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 407, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 408, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 409, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 410, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 411.

Suitable substitutions at amino acid position 20 of the modified hIL-2 portion of the immunoconjugates include, for example, any of a D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitution.

Suitable substitutions at amino acid position 38 of the modified hIL-2 portion of the immunoconjugates include, for example, any of an R38E, R38N, R38G, R38H, R38I, R38L, R38M, R38F, R38P, R38S, R38T, R38W, R38Y, R38V, R38A, R38Q, R38D, or a R38K substitution.

In some embodiments, any one of the D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitutions can be combined with an R38E substitution.

The modified hIL-2 protein portion of the immunoconjugates can comprise the amino acid sequence of any one of SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620. The modified hIL-2 protein portion of the immunoconjugates can comprise the amino acid sequence of any one of SEQ ID NOs: 134-150, 307, 344, 608, 611, 614, or 620. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 134. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 135. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 136. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 137. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 138. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 139. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 140. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 141. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 142. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 143. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 144. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 145. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 146. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 147. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 148. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 149. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 150. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 307. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 344. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 607. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 608. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 609. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 610. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 611. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 614. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 617. In some embodiments, the modified hIL-2 proteins comprise the amino acid sequence of SEQ ID NO: 620. The modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 can further comprise a T3A substitution and/or a C125A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 further comprises a T3A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 further comprises a C125A substitution. In some embodiments, the modified hIL-2 protein of any one of amino acid sequences SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620 further comprises a T3A substitution and a C125A substitution.

The modified hIL-2 protein portion of the immunoconjugates can comprise a D20A substitution and a R38E substitution.

The modified hIL-2 protein portion of the immunoconjugates can further comprise a substitution at amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. A suitable substitution includes, for example, a T3A. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates comprise a T3A substitution, a D20A substitution, and a R38E substitution. In some aspects, the modified hIL-2

protein portion of the immunoconjugates comprise the amino acid sequence of SEQ ID NO: 216.

Alternatively, the modified hIL-2 protein portion of the immunoconjugates can further comprise a deletion of amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates comprise a deletion of amino acids 1-3, a D20A substitution, and a R38E substitution. In some aspects, the modified hIL-2 protein portion of the immunoconjugates comprise the amino acid sequence of SEQ ID NO: 218.

The modified hIL-2 protein portion of the immunoconjugates can further comprise a deletion or substitution at amino acid position 125 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345. The substitution at amino acid position 125 can be C125A. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates comprise a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates comprise the amino acid sequence of SEQ ID NO: 215. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates comprise a T3A substitution, a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates comprise the amino acid sequence of SEQ ID NO: 217. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates comprise a deletion of amino acids 1-3, a D20A substitution, a R38E substitution, and a C125A substitution. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates comprise the amino acid sequence of SEQ ID NO: 219.

The modified hIL-2 protein portion of the immunoconjugates can exhibit a reduction in potency of at least about 200-fold, at least about 500-fold, at least about 1,000-fold, at least about 2,000-fold, at least about 5,000-fold, at least about 6,500-fold, or at least about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) relative to a non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates can exhibit a reduction in potency of greater than about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) relative to a non-modified hIL-2. A greater reduction in hIL-2 potency on the high affinity hIL-2 receptor may be possible and acceptable for the modified hIL-2 proteins described herein, but such a reduction may not be quantifiable with the methods described herein due to limits of the cell proliferation assay conditions.

In addition, the modified hIL-2 protein portion of the immunoconjugates can exhibit a reduction in potency of at least about 200-fold, at least about 500-fold, at least about 1,000-fold, at least about 2,000-fold, at least about 5,000-fold, at least about 6,500-fold, or at least about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to an non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates can exhibit a reduction in potency of greater than about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to an non-modified hIL-2.

The modified hIL-2 protein portion of the immunoconjugates can exhibit a reduction in potency of up to about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) and a reduction in potency of up to about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. The modified hIL-2 protein portion of the immunoconjugates can exhibit a reduction in potency of greater than about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) and a reduction in potency of greater than about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2.

The hIL-2 protein portion of the immunoconjugates can be fused to the antibody or an antigen-binding fragment thereof at the N-terminus of an antibody light chain, the C-terminus of an antibody light chain, the N-terminus of an antibody heavy chain, the C-terminus of an antibody heavy chain, the N-terminus of the antigen-binding fragment, or the C-terminus of the antigen-binding fragment. In some embodiments, the hIL-2 protein portion of the immunoconjugates is directly fused by a peptide bond to the human antibody molecule or an antigen-binding fragment thereof. The hIL-2 protein portion of the immunoconjugates can be, for example, directly fused by a peptide bond to the C-terminal amino acid residue of the antibody heavy chain. In some embodiments, the hIL-2 protein portion of the immunoconjugates is fused to the human antibody molecule or an antigen-binding fragment thereof through a linker.

Fusion of the modified hIL-2 proteins to the human antibody molecules or antigen-binding fragments thereof can rescue the modified hIL-2 proteins' ability to activate the intermediate affinity IL-2 receptor. In some embodiments, the immunoconjugate is able to activate the intermediate affinity IL-2 receptor to a degree that is comparable to wild type hIL-2 activation of the intermediate affinity IL-2 receptor.

In some embodiments, the human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates comprise a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 418, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 419, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 420, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 421, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 422, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 423.

In some embodiments, the human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates comprise a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 386, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 387, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 388, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 389, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 390, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 391.

In some embodiments, the human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates comprise a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 396, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 397, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 398, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 399, a light chain CDR2 comprising the amino acid sequence of SEQ ID

NO: 400, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 401.

In some embodiments, the human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates comprise a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 406, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 407, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 408, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 409, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 410, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 411.

The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates can comprise a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 416 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 417.

The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates can comprise a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 384 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 385.

The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates can comprise a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 394 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 395.

The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates can comprise a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 404 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 405.

The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates can comprise an IgG1 heavy chain constant region.

The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates can have substitutions or deletions within the constant region to minimize Fc-mediated immune effector function, such as FcγRIIIA-mediated antibody-dependent cell-mediated cytotoxicity (ADCC), FcγRI- and FcγRIIa-dependent antibody-dependent cellular phagocytosis (ADCP), and Clq binding-mediated complement-dependent cytotoxicity (CDC). In some embodiments, the human antibody molecule portion of the immunoconjugates comprise a L235A substitution, wherein the amino acid numbering is according to EU numbering. In some embodiments, the human antibody molecule portion of the immunoconjugates comprise a G237A substitution, wherein the amino acid numbering is according to EU numbering. In some embodiments, the human antibody molecule portion of the immunoconjugates comprise an L235A and a G237A substitution, wherein the amino acid numbering is according to EU numbering.

The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates can comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 414 and a light chain comprising the amino acid sequence of SEQ ID NO: 415.

The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates can comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 424 and a light chain comprising the amino acid sequence of SEQ ID NO: 425.

The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates can comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 426 and a light chain comprising the amino acid sequence of SEQ ID NO: 427.

The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugates can comprise a heavy chain comprising the amino acid sequence of SEQ ID NO: 428 and a light chain comprising the amino acid sequence of SEQ ID NO: 429.

The immunoconjugates can have one or more of the following properties:

- Binds to PD-1 but does not inhibit PD-L1 binding to PD-1;
- Binds to PD-1 in the presence of standard-of-care anti-PD-1 antibodies used in the clinic (e.g., KEYTRUDA" and OPDIVOR);
- Is highly selective for PD-1 and does not immunospecifically bind other related B7 family members;
- Binds PD-1 on activated human T cells (EC_{50}~0.1-0.2 nM in a flow binding assay);
- Has reduction in potency of at least about 200-fold, at least about 500-fold, at least about 1,000-fold, at least about 2,000-fold, at least about 5,000-fold, at least about 6,500-fold, or at least about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) relative to a non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates can exhibit a reduction in potency of greater than about 10,000-fold on the high affinity IL-2 receptor (hIL-2Rαβγ) relative to a non-modified hIL-2. A greater reduction in hIL-2 potency on the high affinity hIL-2 receptor may be possible and acceptable for the modified hIL-2 proteins described herein, but such a reduction may not be quantifiable with the methods described herein due to limits of the cell proliferation assay conditions;
- Has a reduction in potency of at least about 200-fold, at least about 500-fold, at least about 1,000-fold, at least about 2,000-fold, at least about 5,000-fold, at least about 6,500-fold, or at least about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to an non-modified hIL-2, for example as quantified by a comparison in EC_{50} values in an hIL-2-dependent cell proliferation assay described herein. In some embodiments, the modified hIL-2 protein portion of the immunoconjugates can exhibit a reduction in potency of greater than about 10,000-fold on the intermediate affinity IL-2 receptor (hIL-2Rβγ) relative to a non-modified hIL-2;
- Rescues and expands PD-1-expressing human memory T cell subsets in a GvHD animal model; and
- Has minimal or no impact on body weight, blood chemistry, or hematology parameters after single dose at 1 and 10 mg/kg in cynomolgus monkeys.

In some embodiments, the immunoconjugate comprises a modified hIL-2 protein comprising a T3A substitution, a R38E substitution, a D20A substitution, and a C125A substitution fused to the C-terminus of the antibody heavy chain of a human anti-hPD-1 antibody comprising a human IgG1 framework with a L235A substitution and a G237A substitution. In some embodiments, the immunoconjugate comprises a light chain comprising the amino acid sequence of

SEQ ID NO: 415 and a heavy chain-hIL-2 protein fusion comprising the amino acid sequence of SEQ ID NO: 532.

The disclosed immunoconjugates can selectively deliver IL-2 signaling to PD-1-expressing T cells. The human antibody molecule, or antigen-binding fragment thereof, portion of the immunoconjugate is utilized solely to deliver the modified hIL-2 to PD-1-expressing cells and does not block PD-1 receptor function, as do classical anti-PD-1 inhibitor antibodies such as OPDIVOR and KEYTRUDAR. The primary mechanism-of-action of the herein disclosed immunoconjugates is via the T cell selective activity of IL-2. The human PD-1 receptor is primarily expressed on a minor subset of T cells with potent tumor reactivity. Without being bound by theory, it is believed that targeting the modified hIL-2 protein portion of the immunoconjugate to this population of T cells can dramatically amplify anti-tumor immunity while reducing or minimizing off-target systemic IL-2-mediated toxicities mediated by cell populations that lack PD-1 expression.

Pharmaceutical Compositions, Polynucleotides, Vectors, and Cells

Disclosed herein are pharmaceutical compositions comprising any of the herein disclosed modified hIL-2 proteins, any of the herein disclosed human antibody molecules or antigen-binding fragments thereof, or any of the herein disclosed immunoconjugates. In some embodiments, the pharmaceutical compositions comprise any of the herein disclosed modified hIL-2 proteins. In some embodiments, the pharmaceutical compositions comprise any of the herein disclosed human antibody molecules or antigen-binding fragments thereof. In some embodiments, the pharmaceutical compositions comprise any of the herein disclosed immunoconjugates.

Disclosed herein are polynucleotides comprising a nucleic acid sequence encoding any of the herein disclosed modified hIL-2 proteins, any of the herein disclosed human antibody molecules or antigen-binding fragments thereof, or any of the herein disclosed immunoconjugates. In some embodiments, the polynucleotides comprise a nucleic acid sequence encoding any of the herein disclosed modified hIL-2 proteins. In some embodiments, the polynucleotides comprise a nucleic acid sequence encoding any of the herein disclosed human antibody molecules or antigen-binding fragments thereof. In some embodiments, the polynucleotides comprise a nucleic acid sequence encoding any of the herein disclosed immunoconjugates.

Disclosed herein are vectors comprising a polynucleotide comprising a nucleic acid sequence that encodes any of the herein disclosed modified hIL-2 proteins, any of the herein disclosed human antibody molecules or antigen-binding fragments thereof, or any of the herein disclosed immunoconjugates. In some embodiments, the vectors comprise a polynucleotide comprising a nucleic acid sequence that encodes any of the herein disclosed modified hIL-2 proteins. In some embodiments, the vectors comprise a polynucleotide comprising a nucleic acid sequence that encodes any of the herein disclosed human antibody molecules or antigen-binding fragments thereof. In some embodiments, the vectors comprise a polynucleotide comprising a nucleic acid sequence that encodes any of the herein disclosed immunoconjugates.

Also disclosed herein are transformed cells comprising any of the herein disclosed vectors.

Methods of Treatment and Uses

Disclosed herein are methods of treating a disease or disorder in a subject, the methods comprising administering a therapeutically effective amount of any of the herein disclosed immunoconjugates or pharmaceutical compositions to the subject to thereby treat the disease.

Also disclosed are uses of any of the herein disclosed immunoconjugates or pharmaceutical compositions in the preparation of a medicament for the treatment of a disease. Also disclosed are uses of any of the herein described immunoconjugates or pharmaceutical compositions for the treatment of a disease or disorder.

The disclosed immunoconjugates and pharmaceutical compositions can be used to treat diseases or disorders in which stimulation of the subject's immune system would be beneficial. In some embodiments, the subject has an insufficient or deficient immune response and the disclosed immunoconjugates and pharmaceutical compositions stimulate the subject's immune response. The antibody portion of the immunoconjugate can serve to direct the modified hIL-2 protein to the subject's immune cells by, for example, binding to an antigen expressed on the surface of the immune cell. In the case of the disclosed modified hIL-2 protein-human anti-hPD-1 antibody immunoconjugates, for example, the anti-PD-1 antibody (or antigen-binding fragment thereof) portion of the immunoconjugate can bind PD-1 expressed on T cells, thereby delivering the modified hIL-2 protein to the T cells. Targeting the modified IL-2 protein to specific cells can dramatically amplify the therapeutic efficacy of the IL-2 protein without off-target systemic toxicities mediated by cell populations that lack the antigen expression. The disclosed methods and uses can be used to treat, for example, cancer, autoimmune diseases and inflammatory diseases, and chronic infections and infectious diseases. Exemplary cancers include bladder cancer, brain cancer, head and neck cancer, pancreatic cancer, lung cancer, non-small cell lung carcinoma, breast cancer, ovarian cancer, uterine cancer, cervical cancer, endometrial cancer, esophageal cancer, colon cancer, colorectal cancer, rectal cancer, gastric cancer, prostate cancer, blood cancer, skin cancer, melanoma, squamous cell carcinoma, bone cancer, and kidney cancer. Exemplary autoimmune diseases and inflammatory disease include systemic lupus erythematosus (SLE), Type 1 diabetes, rheumatoid arthritis, ankylosing spondylitis, psoriasis, Behcet's disease, granulomatosis with polyangiitis, Takayasu's disease, Crohn's disease, ulcerative colitis, autoimmune hepatitis, sclerosing cholangitis, Sjoren's syndrome, alopecia areata, and inflammatory myopathies. Exemplary infectious diseases include HIV and hepatitis B.

In some embodiments, the disease is cancer. The methods and uses can comprise administering a therapeutically effective amount of any of the herein disclosed modified hIL-2 protein-antibody conjugates to the subject to thereby treat the cancer. In some aspects, the cancer is melanoma. In some aspects, the cancer is non-small cell lung carcinoma.

EXAMPLES

The following examples are provided to further describe some of the embodiments disclosed herein. The examples are intended to illustrate, not to limit, the disclosed embodiments.

General Methods

Protocol A. Flow Cytometry Screen for Binding of Anti-hPD-1 Antibodies or Anti-hPD-1 Antibody-Attenuated hIL-2 Fusions to Human PD-1

To test for binding to hPD-1, antibodies and antibody-attenuated hIL-2 fusion proteins were characterized in full titration curves. A Jurkat cell line was transfected with a mammalian vector which encoded amino acids 1-185 of

human PD-1 (SEQ ID NO: 346) to stably express the extracellular domain and a portion of the transmembrane domain of human PD-1, and this transfected cell line was used to determine binding of anti-hPD-1 antibodies. Jurkat+ hPD-1 cells were washed and added to 96-well plates at 100,000 cells per well in FACS buffer (PBS, 0.2% Heat-inactivated Fetal Bovine Serum). Cells were blocked with 1:50 dilution of human FcR Block (Miltenyi) for 10 minutes at 4° C. and washed with FACS buffer.

Antibodies or antibody-attenuated hIL-2 immunoconjugates (fusion proteins) were serially diluted six-fold in FACS buffer for an 8-point curve and added to human PD-1 expressing Jurkat cells for 1 hour on ice in 100 μL volume. Cells were washed and re-suspended in FACS buffer containing 1:40 dilution of Allophycocyanin conjugated anti-human IgG Fc monoclonal antibody. Cells were washed once more, re-suspended in FACS buffer containing 1:1000 dilution of Sytox Green (Thermo Fisher) and flow cytometric analysis was conducted on the BD FACS Canto II, BD Celesta or BD Fortessa (BD Biosciences) flow cytometers. The geometric mean fluorescent intensity (gMFI) was calculated using FlowJo software version 10. Half maximal effective concentration (EC_{50}) values were calculated from the gMFI of the Allophycocyanin signal across the titrated concentrations using GraphPad Prism 7 software.

Protocol B. Flow Cytometry Competition Screen for Binding of Anti-hPD-1 Antibodies or Anti-hPD-1 Antibody-Attenuated hIL-2 Fusions to Human PD-1

Antibodies and antibody-attenuated hIL-2 fusion proteins were tested for the ability to bind human PD-1 in the presence of a saturating concentration of anti-hPD-1 #1-mIgG2b-N297A (sequence comprising the heavy and light chain variable region sequences of nivolumab, clone 5C4, as described in U.S. Patent Pub. No. US 2009/0217401A1, formatted onto a murine IgG2b-N297A background) (SEQ ID NOs: 348 and 349) or anti-hPD-1 #2-mIgG2b-N297A (sequence comprising the heavy and light chain variable region sequences of pembrolizumab (clone 109A-H/K09A-L-11) as described in Int'l Pub. No. WO2008/156712A1, formatted onto a murine IgG2b-N297A background) (SEQ ID NOs: 350 and 351).

Antibodies or antibody-attenuated hIL-2 fusion proteins were serially diluted six-fold for an 8-point titration curve with and without saturating amounts of 10 UM anti-hPD-1 #1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N297A. Briefly, Jurkat cells stably expressing hPD-1 (as described in Protocol A above) were washed and re-suspended in FACS buffer containing 1:50 dilution of human FcR Blocking reagent. Cells were incubated at 4° C. for 10 minutes and washed. Cells were then re-suspended in 100 μL volume with anti-hPD-1 #1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N287A diluted in FACS buffer to 10 UM and incubated at 4° C. for one hour. Cells were washed and incubated with test antibodies or antibody-attenuated hIL-2 fusion proteins serially diluted six-fold for an 8-point curve in 100 μL volume for one hour at 4° C. To detect bound test anti-hPD-1 antibodies or anti-hPD-1-attenuated hIL-2 fusion proteins, cells were washed again and incubated with 1:40 dilution of Allophycocyanin-conjugated anti-human IgG Fc monoclonal antibody for 45 minutes on ice. Cells were washed and re-suspended in FACS buffer containing 1:1000 dilution of Sytox Green (Thermo Fisher). To generate a comparison, Jurkat cells stably expressing human PD-1 were incubated with only the titrated test antibodies or antibody-attenuated hIL-2 fusion proteins (without anti-hPD-1 #1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N297A) and subsequently with 1:40 dilution of Allophycocyanin-conjugated anti-human IgG Fc secondary. As a control, the variable regions of anti-hPD-1 #1 and anti-hPD-1 #2 were cloned into hIgG4 frameworks and were assessed with and without the addition of anti-hPD-1 #1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N297A. Flow cytometry was carried out on the BD Canto II, BD Celesta, or BD Fortessa (BD Biosciences) flow cytometers and gMFI was calculated using FlowJo software version 10. EC_{50} values were calculated from the gMFI of the Allophycocyanin signal across the titrated concentrations using GraphPad Prism 7 software.

Protocol C. Cell-Based Screen for Characterization of Non-Antagonist Anti-hPD-1 Antibodies or Anti-hPD-1 Antibody-Attenuated hIL-2 Fusions

Human PD-1 antibodies and anti-hPD-1-attenuated hIL-2 fusion proteins were characterized for the ability to block hPD-1 from binding to ligand hPD-L1 (SEQ ID NO: 584). Anti-hPD-1 antibodies and anti-hPD-1-attenuated hIL-2 fusion proteins were either characterized as an antagonist or non-antagonist using an in vitro cell-based human PD-1/PD-L1 blockade bioassay (Promega, Cat #J1255). This co-culture assay utilized two cell lines: FCyR11b artificial Antigen Presenting Cells/Chinese Ovary Hamster K1 (aAPC/CHO-K1) and Jurkat Effector cells. aAPC/CHO K1 cells stably express both human PD-L1 ligand and a cell surface protein to activate cognate T cell receptors (TCRs) while Jurkat Effector cells express hPD-1 and a luciferase reporter under the control of Nuclear Factor of Activated T cells response element (NFAT-RE). When these cells are co-cultured in the presence of a non-antagonistic antibody, hPD-1/hPD-L1 interaction inhibits TCR signaling and no luminescence is detected. In the presence of an antibody that antagonizes hPD-1 interaction with hPD-L1 (SEQ ID NO: 584), the inhibitory signal is disrupted and luminescence is detected.

The thaw-and-use assay was performed according to manufacturer's instructions. In short, aAPC/CHO-K1 cells were first thawed and plated at 30,000 cells per well in flat-bottom 96-well plates for 18 hours at 37° C. in a 5% CO_2 incubator. After cells had adhered, the media was removed and 200 nM or 1000 nM test antibodies or antibody-attenuated hIL-2 fusion proteins were diluted in 40 μL assay buffer (RPMI 1640 medium+1% FBS) and added to the aAPC/CHO-K1 cells. A human IgG4 isotype control monoclonal antibody which targeted Keyhole Limpet Hemocyanin (KLH) clone C3 (SEQ ID NOs: 585 and 586) was used as a negative control. Jurkat effector cells expressing hPD-1 were added at 24,000 cells per well in 40 μL volume. The final concentration of fixed antibodies tested was 100 nM or 500 nM. In some examples, a range of concentrations of anti-hPD-11 or anti-hPD-1-attenuated hIL-2 fusion proteins were tested in this co-culture assay, with the top concentration in a five-fold titration series of 500 nM (FIG. 7).

The co-culture assay was incubated at 37° C. in a 5% CO_2 incubator for an additional 18-20 hours. To read the luminescence signal, plates were allowed to come to room temperature, and 80 μL of the Bio-Glo™ reagent was added to each well. The plates were incubated for 15 minutes in the dark at room temperature and luminescence was read on a Victor X luminometer (Perkin Elmer). Relative luminescence units (RLU) were averaged for each triplicate and graphed using GraphPad Prism 7 software.

Protocol D. In Vitro Phosphorylated STAT5 Assay to Test Attenuation of hIL-2 Variants

The level of attenuation of hIL-2 receptor activation activity of antibody-attenuated hIL-2 fusion proteins was characterized using a phosphorylated STAT5 assay. Variants

were tested in both hIL-2 responsive human natural killer NK-92 cells and engineered human erythroleukemic TF1 cells. The NK-92 cell line naturally expresses the high-affinity hIL-2 receptor (IL-2Rαβγ) at physiologic levels, while the TF1 cell line that naturally expresses the IL-2RY (SEQ ID NO: 352) was engineered to also stably express human CD122 (IL-2RB) (SEQ ID NO: 353) for expression of the intermediate affinity hIL-2 receptor complex (IL-2Rβγ). This TF1+IL-2Rβ stable cell line does not express the IL-2Rα(SEQ ID NO: 354). Both NK-92 and TF1+IL-2Rβ cell lines were used to assess the level of attenuation of IL-2 potency in these cell-based potency assays as fixed concentration screens and full titration curves.

To perform the fixed concentration screen, 100,000 NK-92 cells or TF1+IL-2Rβ cells were plated into 96 wells in 50 μL of fresh growth medium lacking human IL-2 cytokine and incubated overnight at 37° C. in a CO_2 incubator. After 15-16 hours, human IL-2 starved cells were treated with 25.7 nM recombinant hIL-2 (denoted as rhIL-2) (SEQ ID NO: 345) or test antibody-attenuated hIL-2 fusion proteins for the NK-92 cell assay, or with 33.3 nM hIL-2 or test hIL-2 variants for the TF1+IL-2Rβ cell assay. Cells were incubated at 37° C., 5% CO_2 for 10 minutes. Cells were fixed with Cytofix Buffer (BD Biosciences) for 10 minutes at 37° C. and then permeabilized after treatment with Perm Buffer III (BD Biosciences) for 30 minutes on ice. hIL-2-dependent Stat5 phosphorylation was detected after staining fixed and permeabilized cells with Alexa Fluor-647 conjugated anti-Stat5 antibody (BD Biosciences) at 0.5 μL per sample for 45 minutes at room temperature in the dark. Cells were washed and reagents were diluted in BD Pharmingen Buffer (BD Biosciences). Stained cells were acquired on a FACS-Celesta cytometer (BD Biosciences) and analyzed using FlowJo software version 10.7.2. The assays were performed in cohorts but normalized using the rhIL-2 for each plate. The degree of attenuation of selected antibody-attenuated hIL-2 fusion proteins were evaluated in an 8-point, 6-fold serially titrated curve ranging from 1200 nM to 7 pM on both NK-92 and TF1+IL-2Rβ cell lines. The procedure for the pStat5 curves was performed in the same manner as the method described above. EC_{50} values were calculated from the geometric mean fluorescent intensity (gMFI) across the titrated concentrations using GraphPad Prism 7 software. The fold change in activity from rhIL-2 was calculated by dividing the EC_{50} values for the variants by the EC_{50} of hIL-2.

Protocol E. In Vitro Cell-Based Proliferation Assay to Test Attenuation of Antibody-Attenuated hIL-2 Fusion Proteins

The antibody-attenuated hIL-2 fusion proteins were also tested for attenuated hIL-2 activity in hIL-2 dependent cell proliferation assays. 10,000 NK-92 cells (expressing the high affinity receptor hIL-2Rαβγ) or TF1+IL-2Rβ cells (expressing the intermediate affinity receptor hIL-2Rβγ) suspended in 50 μL of fresh growth medium without hIL-2 cytokine were plated per well in 96-well U-bottom cell culture plate. Eight point, 6-fold serial titrations of antibody-attenuated hIL-2 fusion proteins with a highest concentration of 996 nM were diluted in fresh media and overlaid on cells in wells. Cells were incubated at 37° C. in a 5% CO_2 incubator for 3 days for TF1+IL-2Rβ cells or 4 days for NK-92 cells. To measure proliferation, Cell-Titer-Glo (Promega) was added to wells, incubated for 10 minutes at room temperature and luminescence was read for 0.1 second per well using a VictorX Multilabel Plate Reader (Perkin Elmer). EC_{50} values were calculated from the relative luminescence units (RLU) across the titrated concentrations using GraphPad Prism 7 software. The fold change in activity from rhIL-2 was calculated by dividing the EC_{50} values for the variants by the EC_{50} of hIL-2. The assays were performed in cohorts but normalized using the rhIL-2 EC_{50} value for each plate.

Example 1: Optimization of Antibody-Attenuated hIL-2 Fusion Protein Variants and Determination of their hIL-2 Activity on the Intermediate and High-Affinity hIL-2 Receptor Complexes

In order to determine the optimal structures for an antibody-attenuated hIL-2 fusion protein, non-attenuated hIL-2 was fused to an anti-DNase I antibody (clone 1H3) designated as 1H3-hIgG1 (SEQ ID NO: 379, SEQ ID NO: 374) in the antibody variable region in a variety of ways as illustrated in FIG. **1**. Variations included the hIL-2 fused at the N-terminus of the human anti-DNase I antibody (clone 1H3) immunoglobulin hIgG1 heavy chain or human kappa light chain via a direct fusion (df) denoted as hIL-2 Nterm light chain df (SEQ ID NO: 379, SEQ ID NO: 356), hIL-2 Nterm heavy chain df (SEQ ID NO: 358, SEQ ID NO: 374) or six amino acid linker (L6) (SEQ ID NO: 355) denoted as hIL-2 Nterm light chain L6 fusion (SEQ ID NO: 379, SEQ ID NO: 357) and hIL-2 Nterm heavy chain L6 fusion (SEQ ID NO: 359, SEQ ID NO: 374). Variations in which the hIL-2 moiety was fused to the C-terminus of both the heavy chains and light chains via df or L6 were also created and denoted as hIL-2 Cterm heavy chain df (SEQ ID NO: 360, SEQ ID NO: 374), hIL-2 Cterm heavy chain L6 fusion (SEQ ID NO: 361, SEQ ID: 374), hIL-2 Cterm light chain df (SEQ ID NO:379, SEQ ID NO: 362), hIL-2 Cterm light chain L6 fusion (SEQ ID NO:379, SEQ ID NO: 363). Further variations were generated in which a CD25/IL-2Rα extracellular domain (amino acids 1-164) (SEQ ID NO: 126) was fused to the N-terminus or C-terminus of the heavy chains or the kappa light chains to interfere with the binding of the IL-2 to CD25 of the IL-2 receptor (FIG. **2**). In these constructs, human CD25 extracellular domain (amino acids 1-164) (SEQ ID NO: 126) was fused to human IL-2 via a 20 amino acid linker (L20) (SEQ ID NO: 364), which was then directly fused or fused via an L6 linker (SEQ ID NO: 355) to 1H3-hIgG1 heavy chain or light chain at the N terminus: hCD25-L20-hIL-2 Nterm heavy chain df (SEQ ID NO: 365, SEQ ID NO: 374), hCD25-L20-hIL-2 Nterm heavy chain L6 fusion (SEQ ID NO: 366, SEQ ID NO: 374), hCD25-L20-hIL-2 Nterm light chain df (SEQ ID NO: 379, SEQ ID NO: 367), hCD25-L20-hIL-2 Nterm light chain L6 fusion (SEQ ID NO: 379, SEQ ID NO: 368). Lastly, a final set of variants in which the CD25/IL-2Rα extracellular domain moiety (SEQ ID NO: 126) fused to the C-terminus of the heavy chain and kappa light chains were created: hCD25-L20-hIL-2 Cterm heavy chain df (SEQ ID NO: 369, SEQ ID NO: 374), hCD25-L20-hIL-2 Cterm heavy chain L6 fusion (SEQ ID NO: 370, SEQ ID NO: 374), hCD25-L20-hIL-2 Cterm light chain df (SEQ ID NO: 379, SEQ ID NO: 371), hCD25-L20-hIL-2 Cterm light chain L6 fusion (SEQ ID NO: 379, SEQ ID NO:372). These antibody-hIL-2 fusion proteins were produced, expressed, and Protein-A purified using standard techniques. The 16 N- or C-terminus and linker variants described above were evaluated in an in vitro cell-based phosphorylated STAT5 assay using an 8-point, 6-fold serial titration, as described in Protocol D.

Table 1 summarizes the EC_{50} calculated over the 8-point, 6-fold serially titrated curves using the geometric mean fluorescence intensity (gMFI) calculated by the FlowJo version 10 software. The fold change from rhIL-2 was also calculated for each variant as a measurement of the level of

attenuation as compared to the activity of the rhIL-2 positive control. Some EC_{50} values were unable to be calculated by the GraphPad Prism 7 software and were marked as Not Calculated (NC); however, based on dose-titration curves there was no attenuation for these variants.

Fusions of the hIL-2 moiety to the N-terminus or C-terminus of the immunoglobulin heavy chain resulted in no reduction in IL-2 activity when compared to rhIL-2 on cell lines expressing the high-affinity hIL-2 receptor (NK-92) or intermediate-affinity hIL-2 receptor (TF1+IL-2RB). The direct fusion (df) of hIL-2 to the antibody component of the fusion protein resulted in no change in IL-2 activity when compared with fusion employing a six amino acid linker (L6) between the IL-2 and antibody components. Similarly, fusions of the IL-2 component to the heavy chain or light chain of the antibody component resulted in no change in IL-2 activity when compared to rhIL-2. All N- or C-terminus and linker fusion protein variants in which the hCD25/hIL-2Rα moiety was fused to hIL-2 were predicted to exhibit reduced binding of the fusion protein to the CD25 of the hIL-2 receptor on cells. Experimentally these constructs exhibited strongly attenuated hIL-2 activity (by at least 45-fold) on the high affinity IL-2 receptor (NK-92) and by 18-fold on the intermediate hIL-2 receptor (TF1+IL-2RB).

TABLE 1

pSTAT5 EC_{50} and fold change on fusion protein domain variants

HC or LC Component Of Fusion Protein	HC and LC SEQ ID NOs:	pSTAT5 EC_{50} (NK-92)	Fold change from rhIL-2 (NK-92)	Attenuation based on dose-titration curves (NK-92)	pSTAT5 EC_{50} (TF1 + IL-2Rβ)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Attenuation based on dose-titration curves (TF1 + IL-2Rβ)
hIL-2 Nterm heavy chain df	358, 374	<0.1 [a]	1[a]	Not Attenuated	1.11	2	Not Attenuated
hIL-2 Nterm heavy chain L6 fusion	359, 374	NC[a]	NC[a]	Not Attenuated	0.19	0	Not Attenuated
hIL-2 Nterm light chain df	379, 356	<0.1 [a]	1[a]	Not Attenuated	0.52	1	Not Attenuated
hIL-2 Nterm light chain L6 fusion	379, 357	<0.1 [a]	0[a]	Not Attenuated	0.13	0	Not Attenuated
hIL-2 Cterm heavy chain df	360, 374	<0.1[a]	0[a]	Not Attenuated	<0.1	0	Not Attenuated
hIL-2 Cterm heavy chain L6 fusion	361, 374	NC[a]	NC[a]	Not Attenuated	<0.1	0	Not Attenuated
hIL-2 Cterm light chain df	379, 362	NC[a]	NC[a]	Not Attenuated	1.15	1	Not Attenuated
hIL-2 Cterm light chain L6 fusion	379, 363	<0.1[a]	0[a]	Not Attenuated	0.25	0	Not Attenuated
hCD25-L20-hIL-2 Nterm heavy chain df	365, 374	7.42	1052	Attenuated	190.50 [a]	314[a]	Attenuated
hCD25-L20-hIL-2 Nterm heavy chain L6 fusion	366, 374	2.24	318	Attenuated	10.70	18	Attenuated
hCD25-L20-hIL-2 Nterm light chain df	379, 367	106.80	15149	Attenuated	328.50 [a]	542[a]	Attenuated
hCD25-L20-hIL-2 Nterm light chain L6 fusion	379, 368	4.45	631	Attenuated	27.88	46	Attenuated
hCD25-L20-hIL-2 Cterm heavy chain df	369, 374	1.89	149	Attenuated	93.89[a]	104[a]	Attenuated
hCD25-L20-hIL-2 Cterm heavy chain L6 fusion	370, 374	6.09	479	Attenuated	90.53[a]	101[a]	Attenuated
hCD25-L20-hIL-2 Cterm light chain df	379, 371	0.58	45	Attenuated	156.90[a]	174[a]	Attenuated
hCD25-L20-hIL-2 Cterm light chain L6 fusion	379, 372	1.76	138	Attenuated	221.90[a]	247[a]	Attenuated

NC = Not Calculated;

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

Example 2: Antibody-Attenuated hIL-2 Fusion Protein Variant Production and Determination of their Binding Kinetics to Recombinant Human CD25 and/or Human CD122

Since there was no reduction in hIL-2 activity in the various N-terminus or C-terminus immunoglobulin heavy chain fusion proteins, the hIL-2 Cterm heavy chain L6 fusion (SEQ ID NOs: 361, 374), designated as "1H3-hIgG1-L6-hIL-2", was used as the base construct for antibody-attenuated-hIL-2 fusion protein variants with substitutions in the hIL-2 moiety. Single, double and/or multiple amino acid substitutions were introduced into selected residues of human IL-2 in order to investigate the role those residues play in the recognition of either human CD25/IL-2Rα and/or human CD122/IL-2Rβ or CD132/IL-2Rγ (human IL-2R subunits). Over three hundred antibody-attenuated hIL-2 fusion protein variants with substitutions in the hIL-2 moiety were generated and evaluated in 6 rounds. These variants were first screened using a flow-based phosphorylated STAT5 (pSTAT5) assay at a fixed concentration on IL-2 dependent cell lines (NK-92 and TF1+IL-2RB) as well as in dose-titration curves. Phosphorylated STAT5 is a downstream signal of IL-2 activity and was used as a snapshot measurement of IL-2 potency. IL-2 dependent cell proliferation assays were also performed to measure IL-2 activity over a period of 3-4 days. Criteria for attenuated hIL-2 selection included: (1) reduced IL-2 potency on both NK-92 and TF1+IL-2Rβ cell lines with greater than 50% agonist activity on both cell lines; and (2) moderate-to-high production yield.

Human anti-DNase I antibody-hIL-2 fusion proteins were generated by fusing the human IL-2 or the human IL-2 variants (SEQ ID NOs: 1-344, 377, 378, and 575) to the C-terminus of a human anti-DNase I antibody (clone 1H3, having a human IgG1 isotype) heavy chain via the L6 linker, which were combined with the hIgG1 light chain (1H3-hkappa LC; SEQ ID NO: 374) to generate the 1H3-hIgG1-L6-hIL-2 fusion proteins (provided in Table 28). Mouse anti-yellow fever virus antibody-hIL-2 fusion proteins were also generated by fusing human IL-2 variants to the C-terminus of a mouse anti-yellow fever virus antibody (clone 2D12, having a mouse IgG1 isotype) heavy chain with a D265A substitution for decreased immune effector function via the L6 linker, which were combined with the 2D12-mIgG1 light chain (2D12-mKappa LC; SEQ ID NO: 376) to generate the 2D12-mIgG1-D265A-L6-hIL-2 fusion proteins (provided in Table 28). Some of these mouse anti-yellow fever virus antibody-hIL-2 fusion proteins were formatted onto a human IgG1 constant region and were generated in the same manner as described above using, which was combined with 2D12-hKappa light chain (2D12-hKappa LC; SEQ ID NO: 573). Iterations of IL-2 amino acid substitutions were performed in six rounds, designated Groups 1 to 6. 1H3-hIgG1-L6-hIL-2, 2D12-mIgG1-D265A-L6-hIL-2, and 2D12-hIgG1-L6-hIL-2 fusion proteins were produced, expressed, and Protein-A purified using standard techniques.

Group 1 contained an initial series of only 2D12-mIgG1-D265A-L6-hIL-2 or 2D12-hIgG1-L6-hIL-2 fusion proteins which comprised a substitution or combination of substitutions in human IL-2 which were predicted to be involved in binding to only one of the IL-2 receptor subunits CD25/IL-2Rα, CD122/IL-2Rβ, or CD132/IL-2Rγ. The fusion proteins in this group included the following substitutions to IL-2 predicted to modulate binding to CD25/IL-2Rα: F42K (SEQ ID NO: 1), V69A (SEQ ID NO: 2), V69E (SEQ ID NO: 3), V69F (SEQ ID NO: 4), V69G (SEQ ID NO: 5), V69H (SEQ ID NO: 6), V69I (SEQ ID NO: 7), V69K (SEQ ID NO: 8), V69L (SEQ ID NO: 9), V69M (SEQ ID NO: 10), V69Q (SEQ ID NO: 11), V69S (SEQ ID NO: 12), V69T (SEQ ID NO: 13), V69W (SEQ ID NO: 14), V69Y (SEQ ID NO: 15), V69R (SEQ ID NO: 581), (F42K/F44K) (SEQ ID NO: 16), (F44K/Y45R) (SEQ ID NO: 17), (F42K/V69R) (SEQ ID NO: 18), (Y45R/V69R) (SEQ ID NO: 19), (F42K/F44K/Y45R) (SEQ ID NO: 20), (F42A/Y45A/L72G) (SEQ ID NO: 574), (R38A/F42K/Y45R) (SEQ ID NO: 21), (R38E/F42K/Y45R) (SEQ ID NO: 22), (K43E/F42K/Y45R) (SEQ ID NO: 23), (K43T/F42K/Y45R) (SEQ ID NO: 24), (F42K/Y45R/E62A) (SEQ ID NO: 25), (P65R/F42K/Y45R) (SEQ ID NO: 26), (P65S/F42K/Y45R) (SEQ ID NO: 27), (V69A/F42K/Y45R) (SEQ ID NO: 28), (V69D/F42K/Y45R) (SEQ ID NO: 29), or (V69R/F42K/Y45R) (SEQ ID NO: 30). The substitutions in this group included the following substitutions predicted to modulate binding to CD122/IL-2RB: D20A (SEQ ID NO: 31), D20N (SEQ ID NO: 32), D20K (SEQ ID NO: 33), N88A (SEQ ID NO: 34), N88G (SEQ ID NO: 35), N88H (SEQ ID NO: 36), N88K (SEQ ID NO: 37), (D20A/D84A) (SEQ ID NO: 38), (D20A/E15A) (SEQ ID NO: 39), (D20A/E95A) (SEQ ID NO: 40), (D20A/N88A) (SEQ ID NO: 41), (D20A/S87A) (SEQ ID NO: 42), (D84A/N88A) (SEQ ID NO: 43), (E15A/N88A) (SEQ ID NO: 44), or (S87A/N88A) (SEQ ID NO: 45). Group 1 also included the following substitutions to IL-2 predicted to modulate IL-2 binding to CD132/IL-2-Rγ: Q126L (SEQ ID NO: 377) or Q126E (SEQ ID NO: 378). The IL-2 substitutions studied in Group 1 were not predicted to modulate binding to more than one of the IL-2 receptor subunits.

Group 2 contained a series of 1H3-hIgG1-L6-hIL-2 fusion proteins which comprised one or more substitutions in human IL-2 which were predicted to be involved in CD25/IL-2Rαbinding only. The fusion proteins in this group included the following substitutions to IL-2 predicted to modulate binding to CD25/IL-2Rα: R38A (SEQ ID NO: 46), R38D (SEQ ID NO: 47), R38E (SEQ ID NO: 48), R38Q (SEQ ID NO: 49), F42R (SEQ ID NO: 50), F42A (SEQ ID NO: 51), F42D (SEQ ID NO: 52), F42H (SEQ ID NO: 53), K43A (SEQ ID NO: 54), K43E (SEQ ID NO: 55), K43Q (SEQ ID NO: 56), Y45A (SEQ ID NO: 57), Y45K (SEQ ID NO: 58), Y45S (SEQ ID NO: 59), Y45R (SEQ ID NO: 60), E61A (SEQ ID NO: 61), E61R (SEQ ID NO: 62), E61K (SEQ ID NO: 63), E62A (SEQ ID NO: 64), E62R (SEQ ID NO: 65), E62K (SEQ ID NO: 66), E62Y (SEQ ID NO: 67), E68Y (SEQ ID NO: 68), E68A (SEQ ID NO: 69), E68K (SEQ ID NO: 70), E68R (SEQ ID NO: 71), E68L (SEQ ID NO: 72), L72Y (SEQ ID NO: 73), L72R (SEQ ID NO: 74), L72A (SEQ ID NO: 75), L72D (SEQ ID NO: 76), L72H (SEQ ID NO: 77), L72F (SEQ ID NO: 78), (R38D/E61R) (SEQ ID NO: 79), (R38D/E61R/K43E) (SEQ ID NO: 80), or (T3A/F42A/Y45A/L72G/C125A) (SEQ ID NO: 81). The substitution T3A was introduced into the IL-2 amino acid sequence to remove the predicted O-linked glycosylation site on human IL-2 (see for example Int'l Pub. No. WO2012/107417) and the substitution C125A was introduced into the IL-2 amino acid sequence to remove an unpaired cysteine residue (see for example Int'l Pub. No. WO2018/184964). The IL-2 substitutions studied in Group 2 were predicted to not modulate IL-2 binding to CD132/IL-2-Rγ, nor were these substitutions predicted to modulate binding to more than one of the IL-2 receptor subunits.

Group 3 contained a series of 1H3-hIgG1-L6-hIL-2 fusion proteins which comprised one or more substitutions in human IL-2 which were predicted to be involved in

CD122/IL-2Rβ binding only. The fusion proteins in this group included the following substitutions to IL-2 predicted to modulate binding to CD122/IL-2RB: E15A (SEQ ID NO: 82), E15R (SEQ ID NO: 83), E15K (SEQ ID NO: 84), H16A (SEQ ID NO: 85), H16Y (SEQ ID NO: 86), H16E (SEQ ID NO: 87), L19A (SEQ ID NO: 88), D20I (SEQ ID NO: 89), D20S (SEQ ID NO: 90), D20H (SEQ ID NO: 91), D20T (SEQ ID NO: 92), D20W (SEQ ID NO: 93), D20Y (SEQ ID NO: 94), D20R (SEQ ID NO: 95), D20F (SEQ ID NO: 96), R81A (SEQ ID NO: 97), D84A (SEQ ID NO: 98), D84R (SEQ ID NO: 99), D84K (SEQ ID NO: 100), S87A (SEQ ID NO: 101), N88Y (SEQ ID NO: 102), N88D (SEQ ID NO: 103), N88R (SEQ ID NO: 104), N88E (SEQ ID NO: 10^5), N88F (SEQ ID NO: 106), N88I (SEQ ID NO: 107), 192A (SEQ ID NO: 108), 192Y (SEQ ID NO: 109), 192S (SEQ ID NO: 110), 192F (SEQ ID NO: 111), 192R (SEQ ID NO: 112), 192D (SEQ ID NO: 113), 192E (SEQ ID NO: 114), E95A (SEQ ID NO: 115), E95R (SEQ ID NO: 116), E95K (SEQ ID NO: 117), (D20Y/H16E) (SEQ ID NO: 118), (D20Y/H16A) (SEQ ID NO: 119), (D20Y/H16Y) (SEQ ID NO: 120), (D20Y/192A) (SEQ ID NO: 121), (D20Y/192S) (SEQ ID NO: 122), (D20Y/192R) (SEQ ID NO: 123), (D20Y/E95R) (SEQ ID NO: 124), or (D20Y/E95A) (SEQ ID NO: 125).

Group 4 contained a series of fusion proteins containing the 1H3-hIgG1-L6-hIL-2 HC fused to a CD25/IL-2Rα extracellular domain moiety (SEQ ID NO: 126), a 20 amino acid linker (L20) (SEQ ID NO: 364), and human IL-2 variants comprising one or more substitutions to residues predicted to be involved in binding to CD122/IL-2Rβ. The fusion proteins in this group included the following substitutions to IL-2 predicted to modulate binding to CD122/IL-2Rβ: E15A (SEQ ID NO: 82), D20I (SEQ ID NO: 89), D20S (SEQ ID NO: 90), D20H (SEQ ID NO: 91), D20W (SEQ ID NO: 93), D20Y (SEQ ID NO: 94), D20R (SEQ ID NO: 95), D20F (SEQ ID NO: 96), D84K (SEQ ID NO: 100), S87A (SEQ ID NO: 101), N88Y (SEQ ID NO: 102), N88D (SEQ ID NO: 103), N88R (SEQ ID NO: 104), N88E (SEQ ID NO: 10^5), N88F (SEQ ID NO: 106), N88I (SEQ ID NO: 107), 192A (SEQ ID NO: 108), E95A (SEQ ID NO: 115), or E95K (SEQ ID NO: 117). The antibody-attenuated hIL-2 fusion proteins in this group are denoted as 1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2.

Group 5 contained a series of 1H3-hIgG1-L6-hIL-2 which comprised a combination of substitutions in IL-2 which were predicted to be involved in binding of IL-2 to CD25/IL-2Rα and to CD122/IL-2Rβ or CD132/IL-2Rγ. In addition, some variants had a deletion in the first three amino acids at the N-terminus of the hIL-2 moiety (Δ1-3APT). The fusion proteins in Group 5 included the following substitutions to IL-2 predicted to modulate IL-2 binding to CD25/IL-2Rα and to CD122/IL-2Rβ: (F42D/D20A) (SEQ ID NO: 127), (F42R/D20A) (SEQ ID NO: 128), (F42K/D20A) (SEQ ID NO: 129), (F42A/D20A) (SEQ ID NO: 130), (F42H/D20A) (SEQ ID NO: 131), (Y45R/D20A) (SEQ ID NO: 132), (Y45K/D20A) (SEQ ID NO: 133), (R38N/D20A) (SEQ ID NO: 134), (R38G/D20A) (SEQ ID NO: 135), (R38H/D20A) (SEQ ID NO: 136), (R38I/D20A) (SEQ ID NO: 137), (R38L/D20A) (SEQ ID NO: 138), (R38M/D20A) (SEQ ID NO: 139), (R38F/D20A) (SEQ ID NO: 140), (R38P/D20A) (SEQ ID NO: 141), (R38S/D20A) (SEQ ID NO: 142), (R38T/D20A) (SEQ ID NO: 143), (R38W/D20A) (SEQ ID NO: 144), (R38Y/D20A) (SEQ ID NO: 145), (R38V/D20A) (SEQ ID NO: 146), (R38A/D20A) (SEQ ID NO: 147), (R38Q/D20A) (SEQ ID NO: 148), (D20A/R38E) (SEQ ID NO: 149), (R38D/D20A) (SEQ ID NO: 150), (K43E/D20A) (SEQ ID NO: 151), (E61A/D20A) (SEQ ID NO: 152), (E62A/D20A) (SEQ ID NO: 153), (E62Y/D20A) (SEQ ID NO: 154), (L72D/D20A) (SEQ ID NO: 155), (L72H/D20A) (SEQ ID NO: 156), (L72R/D20A) (SEQ ID NO: 157), (F42D/192D) (SEQ ID NO: 158), (F42R/192D) (SEQ ID NO: 159), (F42H/192D) (SEQ ID NO: 160), (F42A/192D) (SEQ ID NO: 161), (H16A/F42A) (SEQ ID NO: 575), (K43E/192D) (SEQ ID NO: 162), (Y45R/192D) (SEQ ID NO: 163), (Y45K/192D) (SEQ ID NO: 164), (E62A/192D) (SEQ ID NO: 165), (E62Y/192D) (SEQ ID NO: 166), (L72D/192D) (SEQ ID NO: 167), (L72H/192D) (SEQ ID NO: 168), (L72R/192D) (SEQ ID NO: 169), (R38D/192D) (SEQ ID NO: 170), (R38E/192D) (SEQ ID NO: 171), (R38Q/192D) (SEQ ID NO: 172), (R38A/192D) (SEQ ID NO: 173), (R38E/N88R) (SEQ ID NO: 174), (R38E/D84R) (SEQ ID NO: 175), (R38E/D84K) (SEQ ID NO: 176), (F42A/Y45R/D20A) (SEQ ID NO: 177), (F42H/Y45R/D20A) (SEQ ID NO: 178), (R38D/E61R/D20A) (SEQ ID NO: 179), (R38E/E61R/D20A) (SEQ ID NO: 180), (R38Q/E61R/D20A) (SEQ ID NO: 181), (R38A/E61R/D20A) (SEQ ID NO: 182), (R38A/D20A/E95A) (SEQ ID NO: 183), (D20A/E95A/R38D) (SEQ ID NO: 184), (D20A/E95A/R38E) (SEQ ID NO: 185), (D20A/E95A/R38Q) (SEQ ID NO: 186), (D20A/E95A/F42R) (SEQ ID NO: 187), (D20A/E95A/F42A) (SEQ ID NO: 188), (D20A/E95A/F42D) (SEQ ID NO: 189), (D20A/E95A/F42H) (SEQ ID NO: 190), (D20A/E95A/F42K) (SEQ ID NO: 191), (D20A/E95A/K43A) (SEQ ID NO: 192), (D20A/E95A/K43E) (SEQ ID NO: 193), (D20A/E95A/K43Q) (SEQ ID NO: 194), (D20A/E95A/Y45A) (SEQ ID NO: 195), (D20A/E95A/Y45K) (SEQ ID NO: 196), (D20A/E95A/Y45S) (SEQ ID NO: 197), (D20A/E95A/Y45R) (SEQ ID NO: 198), (D20A/E95A/E61A) (SEQ ID NO: 199), (D20A/E95A/E62A) (SEQ ID NO: 200), (D20A/E95A/E62R) (SEQ ID NO: 201), (D20A/E95A/E62K) (SEQ ID NO: 202), (D20A/E95A/E62Y) (SEQ ID NO: 203), (D20A/E95A/E68Y) (SEQ ID NO: 204), (D20A/E95A/E68A) (SEQ ID NO: 205), (D20A/E95A/E68L) (SEQ ID NO: 206), (D20A/E95A/L72Y) (SEQ ID NO: 207), (D20A/E95A/L72R) (SEQ ID NO: 208), (D20A/E95A/L72A) (SEQ ID NO: 209), (D20A/E95A/L72D) (SEQ ID NO: 210), (D20A/E95A/L72H) (SEQ ID NO: 211), (D20A/E95A/L72F) (SEQ ID NO: 212), (F42K/Y45R/D20A/S87A) (SEQ ID NO: 213), (F42K/Y45R/D20A/E95A) (SEQ ID NO: 214), (D20A/R38E/C125A) (SEQ ID NO: 215), (T3A/D20A/R38E) (SEQ ID NO: 216), (T3A/D20A/R38E/C125A) (SEQ ID NO: 217), (Δ-3APT/D20A/R38E) (SEQ ID NO: 218), or (Δ-3APT/D20A/R38E/C125A) (SEQ ID NO: 219). The fusion proteins in Group 5 included the following substitutions to IL-2 predicted to modulate IL-2 binding to CD25/IL-2Rα and to CD132/IL-2R: (R38E/Q22A) (SEQ ID NO: 220), (R38E/T123A) (SEQ ID NO: 221), (R38E/1129A) (SEQ ID NO: 222), (R38E/S130A) (SEQ ID NO: 223), (R38E/Q126A) (SEQ ID NO: 224), (R38E/Q126D) (SEQ ID NO: 225), (R38E/Q126V) (SEQ ID NO: 226), (R38E/Q22A/S130A) (SEQ ID NO: 227), (F42K/Y45R/Q126D) (SEQ ID NO: 228), or (D20A/E95A/Q126D) (SEQ ID NO: 229). Mutations to the hIL-2 sequence for Group 5 antibody-attenuated hIL-2 fusion proteins in which the numbering is according to IL-2 sequence are listed in SEQ ID NO: 127-229 and 575.

Group 6 contained a series of 1H3-hIgG1-L6-hIL-2 fusion proteins which comprised a combination of substitutions in human IL-2 which were predicted to be involved in binding of IL-2 to CD25/IL-2Rα and to CD122/IL-2Rβ, but not to CD132/IL-2Rγ. The fusion proteins in Group 6 included the following combination of substitutions in IL-2 predicted to modulate IL-2 binding to CD25/IL-2Rα and

CD122/IL-2Rβ: (D20A/E61R) (SEQ ID NO: 230), (D20A/E61N) (SEQ ID NO: 231), (D20A/E61D) (SEQ ID NO: 232), (D20A/E61Q) (SEQ ID NO: 233), (D20A/E61G) (SEQ ID NO: 234), (D20A/E61H) (SEQ ID NO: 235), (D20A/E61I) (SEQ ID NO: 236), (D20A/E61L) (SEQ ID NO: 237), (D20A/E61K) (SEQ ID NO: 238), (D20A/E61M) (SEQ ID NO: 239), (D20A/E61F) (SEQ ID NO: 240), (D20A/E61P) (SEQ ID NO: 241), (D20A/E61S) (SEQ ID NO: 242), (D20A/E61T) (SEQ ID NO: 243), (D20A/E61W) (SEQ ID NO: 244), (D20A/E61Y) (SEQ ID NO: 245), (D20A/E61V) (SEQ ID NO: 246), (D20A/F42N) (SEQ ID NO: 247), (D20A/F42Q) (SEQ ID NO: 248), (D20A/F42E) (SEQ ID NO: 249), (D20A F42G) (SEQ ID NO: 250), (D20A/F42I) (SEQ ID NO: 251), (D20A/F42L) (SEQ ID NO: 252), (D20A/F42M) (SEQ ID NO: 253), (D20A/F42P) (SEQ ID NO: 254), (D20A/F42S) (SEQ ID NO: 255), (D20A/F42T) (SEQ ID NO: 256), (D20A/F42W) (SEQ ID NO: 257), (D20A/F42Y) (SEQ ID NO: 258), (D20A/F42V) (SEQ ID NO: 259), (D20A/Y45A) (SEQ ID NO: 260), (D20A/Y45N) (SEQ ID NO: 261), (D20A/Y45D) (SEQ ID NO: 262), (D20A/Y45Q) (SEQ ID NO: 263), (D20A/Y45E) (SEQ ID NO: 264), (D20A/Y45G) (SEQ ID NO: 265), (D20A/Y45H) (SEQ ID NO: 266), (D20A/Y45I) (SEQ ID NO: 267), (D20A/Y45L) (SEQ ID NO: 268), (D20A/Y45M) (SEQ ID NO: 269), (D20A/Y45F) (SEQ ID NO: 270), (D20A/Y45P) (SEQ ID NO: 271), (D20A/Y45S) (SEQ ID NO: 272), (D20A/Y45T) (SEQ ID NO: 273), (D20A/Y45W) (SEQ ID NO: 274), (D20A/Y45V) (SEQ ID NO: 275), (192D/F42N) (SEQ ID NO: 276), (192D/F42Q) (SEQ ID NO: 277), (192D/F42E) (SEQ ID NO: 278), (192D/F42G) (SEQ ID NO: 279), (192D/F42I) (SEQ ID NO: 280), (192D/F42L) (SEQ ID NO: 281), (192D/F42K) (SEQ ID NO: 282), (192D/F42M) (SEQ ID NO: 283), (192D/F42P) (SEQ ID NO: 284), (192D/F42S) (SEQ ID NO: 285), (192D/F42T) (SEQ ID NO: 286), (192D/F42W) (SEQ ID NO: 287), (192D/F42Y) (SEQ ID NO: 288), (192D/F42V) (SEQ ID NO: 289), (192D/Y45A) (SEQ ID NO: 290), (192D/Y45N) (SEQ ID NO: 291), (192D/Y45D) (SEQ ID NO: 292), (192D/Y45Q) (SEQ ID NO: 293), (192D/Y45E) (SEQ ID NO: 294), (192D/Y45G) (SEQ ID NO: 295), (192D/Y45H) (SEQ ID NO: 296), (192D/Y451) (SEQ ID NO: 297), (192D/Y45L) (SEQ ID NO: 298), (192D/Y45M) (SEQ ID NO: 299), (192D/Y45F) (SEQ ID NO: 300), (192D/Y45P) (SEQ ID NO: 301), (192D/Y45S) (SEQ ID NO: 302), (192D/Y45T) (SEQ ID NO: 303), (192D/Y45W) (SEQ ID NO: 304), (192D/Y45V) (SEQ ID NO: 305), (R38E/D20H) (SEQ ID NO: 306), (R38E/D20S) (SEQ ID NO: 307), (F42A/N88R) (SEQ ID NO: 308), (F42A/N88D) (SEQ ID NO: 309), (R38E/D84A) (SEQ ID NO: 310), (R38E/D84N) (SEQ ID NO: 311), (R38E/D84Q) (SEQ ID NO: 312), (R38E/D84E) (SEQ ID NO: 313), (R38E/D84G) (SEQ ID NO: 314), (R38E/D84H) (SEQ ID NO: 315), (R38E/D84I) (SEQ ID NO: 316), (R38E/D84L) (SEQ ID NO: 317), (R38E/D84M) (SEQ ID NO: 318), (R38E/D84F) (SEQ ID NO: 319), (R38E/D84P) (SEQ ID NO: 320), (R38E/D84S) (SEQ ID NO: 321), (R38E/D84T) (SEQ ID NO: 322), (R38E/D84W) (SEQ ID NO: 323), (R38E/D84Y) (SEQ ID NO: 324), (R38E/D84V) (SEQ ID NO: 325), (R38E/192A) (SEQ ID NO: 326), (R38E/192R) (SEQ ID NO: 327), (R38E/192N) (SEQ ID NO: 328), (R38E/192Q) (SEQ ID NO: 329), (R38E/192E) (SEQ ID NO: 330), (R38E/192G) (SEQ ID NO: 331), (R38E/192H) (SEQ ID NO: 332), (R38E/192L) (SEQ ID NO: 333), (R38E/192K) (SEQ ID NO: 334), (R38E/192M) (SEQ ID NO: 335), (R38E/192F) (SEQ ID NO: 336), (R38E/192P) (SEQ ID NO: 337), (R38E/192S) (SEQ ID NO: 338), (R38E/192T) (SEQ ID NO: 339), (R38E/192W) (SEQ ID NO: 340), (R38E/192Y) (SEQ ID NO: 341), (R38E/192V) (SEQ ID NO: 342), (R38E/H16E) (SEQ ID NO: 343), or (R38K/D20A) (SEQ ID NO: 344). Mutations to the hIL-2 sequence for Group 6 antibody-attenuated hIL-2 fusion proteins in which the numbering is according to IL-2 sequence is listed in SEQ ID NO: 230-344.

The binding kinetics of some purified 1H3-hIgG1-L6-hIL-2 variant proteins for individual recombinant human CD25 and human CD122 were determined using bio-layer interferometry (BLI). Briefly, binding experiments were performed using an Octet Red96 instrument (Pall ForteBio) at 25° C. C-terminal poly-histidine tagged human CD25 and human CD122 extracellular domains were captured onto anti-His2 sensors (Pall ForteBio). Receptor loaded sensors were dipped into a 7-point serial 3-fold dilution of each 1H3-hIgG-L6-hIL-2 variant, starting at a top concentration of 300 nM. 1H3-hIgG1-L6-hIL-2 fusion proteins were diluted into an assay buffer consisting of phosphate buffered saline (PBMS) supplemented with 0.1% BSA, 0.02% Tween-20 (pH 7.2). Loaded sensors were regenerated using 10 mM Glycine buffer (pH 1.7). Kinetic constants were calculated using a monovalent binding model.

Table 2 documents the association constant (kon), dissociation constant (koff), and equilibrium constant (K_D) of 74 immunoglobulin-hIL-2 fusion protein variants bound to recombinant human CD25 or recombinant human CD122.

TABLE 2

Binding kinetics of 1H3-hIgG-L6-hIL-2 fusion proteins to recombinant human CD25 or CD122 by Octet BLI

1H3-hIgG1-L6-hIL-2 fusion proteins	SEQ ID NO of hIL-2 variant	Predicted receptor sub-unit targeted by IL-2 substitution	K_D (M)	k_{on} (1/Ms)	k_{off} (1/s)
1H3-hIgG1-L6-hIL-2 WT	345	N/A	3.20E−10	5.90E+05	1.90E−04
1H3-hIgG1-L6-hIL-2 (E15A)	82	CD122	2.04E−09	1.15E+05	2.35E−04
1H3-hIgG1-L6-hIL-2 (E15R)	83	CD122	3.41E−09	9.48E+04	3.23E−04
1H3-hIgG1-L6-hIL-2 (E15K)	84	CD122	1.39E−09	1.71E+05	2.37E−04
1H3-hIgG1-L6-hIL-2 (H16A)	85	CD122	1.68E−09	1.71E+05	2.87E−04
1H3-hIgG1-L6-hIL-2 (H16Y)	86	CD122	1.46E−09	1.50E+05	2.20E−04
1H3-hIgG1-L6-hIL-2 (H16E)	87	CD122	1.40E−09	1.57E+05	2.20E−04

TABLE 2-continued

Binding kinetics of 1H3-hIgG-L6-hIL-2 fusion proteins to recombinant human CD25 or CD122 by Octet BLI

1H3-hIgG1-L6-hIL-2 fusion proteins	SEQ ID NO of hIL-2 variant	Predicted receptor sub-unit targeted by IL-2 substitution	K_D (M)	k_{on} (1/Ms)	k_{off} (1/s)
1H3-hIgG1-L6-hIL-2 (L19A)	88	CD122	1.76E−09	2.03E+05	3.57E−04
1H3-hIgG1-L6-hIL-2 (D20I)	89	CD122	1.16E−09	1.70E+05	1.98E−04
1H3-hIgG1-L6-hIL-2 (D20S)	90	CD122	6.24E−10	1.74E+05	1.09E−04
1H3-hIgG1-L6-hIL-2 (D20H)	91	CD122	1.13E−09	1.88E+05	2.12E−04
1H3-hIgG1-L6-hIL-2 (D20W)	93	CD122	1.01E−09	1.87E+05	1.90E−04
1H3-hIgG1-L6-hIL-2 (D20Y)	94	CD122	1.42E−09	1.51E+05	2.14E−04
1H3-hIgG1-L6-hIL-2 (D20R)	95	CD122	1.21E−09	1.44E+05	1.75E−04
1H3-hIgG1-L6-hIL-2 (D20F)	96	CD122	1.57E−09	1.75E+05	2.75E−04
1H3-hIgG1-L6-hIL-2 (R38A)	46	CD25	5.55E−09	1.82E+05	1.01E−03
1H3-hIgG1-L6-hIL-2 (R38D)	47	CD25	1.86E−09	8.84E+05	1.64E−03
1H3-hIgG1-L6-hIL-2 (R38E)	48	CD25	8.74E−09	3.31E+05	2.89E−03
1H3-hIgG1-L6-hIL-2 (R38Q)	49	CD25	6.33E−09	4.83E+05	3.05E−03
1H3-hIgG1-L6-hIL-2 (F42R)	50	CD25	2.63E−09	1.59E+06	4.20E−03
1H3-hIgG1-L6-hIL-2 (F42A)	51	CD25	9.25E−09	9.89E+05	9.15E−03
1H3-hIgG1-L6-hIL-2 (F42D)	52	CD25	4.51E−09	1.70E+06	7.64E−03
1H3-hIgG1-L6-hIL-2 (F42H)	53	CD25	6.84E−09	8.23E+05	5.63E−03
1H3-hIgG1-L6-hIL-2 (K43A)	54	CD25	4.79E−09	2.59E+05	1.24E−03
1H3-hIgG1-L6-hIL-2 (K43E)	55	CD25	5.66E−09	4.52E+05	2.56E−03
1H3-hIgG1-L6-hIL-2 (K43Q)	56	CD25	2.28E−09	4.49E+05	1.02E−03
1H3-hIgG1-L6-hIL-2 (Y45A)	57	CD25	3.66E−09	4.29E+05	1.57E−03
1H3-hIgG1-L6-hIL-2 (Y45K)	58	CD25	9.03E−09	5.22E+05	4.71E−03
1H3-hIgG1-L6-hIL-2 (Y45S)	59	CD25	2.45E−09	5.05E+05	1.24E−03
1H3-hIgG1-L6-hIL-2 (Y45R)	60	CD25	1.96E−09	6.46E+05	1.27E−03
1H3-hIgG1-L6-hIL-2 (E61A)	61	CD25	7.00E−09	3.21E+05	2.25E−03
1H3-hIgG1-L6-hIL-2 (E61R)	62	CD25	8.84E−09	1.22E+06	1.08E−02
1H3-hIgG1-L6-hIL-2 (E61K)	63	CD25	1.56E−08	3.16E+05	4.94E−03
1H3-hIgG1-L6-hIL-2 (E62A)	64	CD25	1.23E−08	3.79E+05	4.67E−03
1H3-hIgG1-L6-hIL-2 (E62R)	65	CD25	No binding observed		
1H3-hIgG1-L6-hIL-2 (E62K)	66	CD25	No binding observed		
1H3-hIgG1-L6-hIL-2 (E62Y)	67	CD25	1.55E−08	2.91E+05	4.50E−03
1H3-hIgG1-L6-hIL-2 (E68Y)	68	CD25	8.18E−09	1.80E+05	1.47E−03
1H3-hIgG1-L6-hIL-2 (E68A)	69	CD25	4.49E−09	1.45E+05	6.52E−04
1H3-hIgG1-L6-hIL-2 (E68K)	70	CD25	9.63E−09	2.54E+05	2.44E−03
1H3-hIgG1-L6-hIL-2 (E68R)	71	CD25	1.16E−08	2.54E+05	2.96E−03
1H3-hIgG1-L6-hIL-2 (E68L)	72	CD25	8.62E−09	1.02E+05	8.82E−04
1H3-hIgG1-L6-hIL-2 (I92R)	112	CD122	2.54E−09	1.08E+05	2.76E−04

TABLE 2-continued

Binding kinetics of 1H3-hIgG-L6-hIL-2 fusion proteins to recombinant human CD25 or CD122 by Octet BLI

1H3-hIgG1-L6-hIL-2 fusion proteins	SEQ ID NO of hIL-2 variant	Predicted receptor sub-unit targeted by IL-2 substitution	K_D (M)	k_{on} (1/Ms)	k_{off} (1/s)
1H3-hIgG1-L6-hIL-2 (I92D)	113	CD122	7.94E−09	4.95E+04	3.93E−04
1H3-hIgG1-L6-hIL-2 (I92E)	114	CD122	2.41E−09	8.54E+04	2.06E−04
1H3-hIgG1-L6-hIL-2 (E95A)	115	CD122	3.11E−09	1.47E+05	4.58E−04
1H3-hIgG1-L6-hIL-2 (E95R)	116	CD122	2.29E−09	1.14E+05	2.61E−04
1H3-hIgG1-L6-hIL-2 (E95K)	117	CD122	3.25E−09	1.25E+05	4.07E−04
1H3-hIgG1-L6-hIL-2 (F42K/Y45R/D20A/S87A)	213	CD25 + CD122	3.25E−08	1.24E+05	4.05E−03
1H3-hIgG1-L6-hIL-2 (F42K/Y45R/D20A/E95A)	214	CD25 + CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (F42K/Y45R/Q126D)	228	CD25 + CD132	No binding observed		
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Q126D)	229	CD122 + CD132	3.34E−09	4.87E+04	1.62E−04
1H3-hIgG1-L6-hIL-2 (R38D/E61R)	79	CD25	No binding observed		
1H3-hIgG1-L6-hIL-2 (R38D/E61R/K43E)	80	CD25	No binding observed		

Table 3 documents the association (kon) constants, dissociation (kofr) constants, and equilibrium constants (K_D)) of 74 1H3-hIgG1-L6-hIL-2 fusion proteins bound to recombinant human CD122.

TABLE 3

Binding kinetics of 1H3-hIgG-L6-hIL-2 fusion proteins to recombinant human CD122 by Octet BLI

1H3-hIgG-L6-hIL-2 fusion proteins	SEQ ID NO of hIL-2 variant	Predicted receptor sub-unit targeted by IL-2 substitution	K_D (M)	k_{on} (1/Ms)	k_{off} (1/s)
1H3-hIgG1-L6-hIL-2 WT	345[a]	N/A	5.60E−09	7.00E+05	3.90E−03
1H3-hIgG1-L6-hIL-2 (E15A)	82[b]	CD122	8.89E−09	1.75E+05	1.56E−03
1H3-hIgG1-L6-hIL-2 (E15R)	83	CD122	3.69E−09	1.46E+05	5.38E−04
1H3-hIgG1-L6-hIL-2 (E15K)	84	CD122	3.56E−09	2.42E+05	8.62E−04
1H3-hIgG1-L6-hIL-2 (H16A)	85	CD122	1.78E−09	1.55E+06	2.76E−03
1H3-hIgG1-L6-hIL-2 (H16Y)	86	CD122	4.36E−09	9.97E+05	4.35E−03
1H3-hIgG1-L6-hIL-2 (H16E)	87	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (L19A)	88	CD122	1.03E−08	4.72E+05	4.87E−03
1H3-hIgG1-L6-hIL-2 (D20I)	89	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (D20S)	90	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (D20H)	91	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (D20W)	93	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (D20Y)	94	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (D20R)	95	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (D20F)	96	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (R38A)	46	CD25	1.38E−08	2.08E+05	2.87E−03

TABLE 3-continued

Binding kinetics of 1H3-hIgG-L6-hIL-2 fusion proteins to recombinant human CD122 by Octet BLI

1H3-hIgG-L6-hIL-2 fusion proteins	SEQ ID NO of hIL-2 variant	Predicted receptor sub-unit targeted by IL-2 substitution	K_D (M)	k_{on} (1/Ms)	k_{off} (1/s)
1H3-hIgG1-L6-hIL-2 (R38D)	47	CD25	2.20E−09	4.28E+05	9.42E−04
1H3-hIgG1-L6-hIL-2 (R38E)	48	CD25	5.81E−09	4.64E+05	2.69E−03
1H3-hIgG1-L6-hIL-2 (R38Q)	49	CD25	1.01E−09	2.81E+05	2.84E−04
1H3-hIgG1-L6-hIL-2 (F42R)	50	CD25	5.47E−09	5.42E+05	2.96E−03
1H3-hIgG1-L6-hIL-2 (F42A)	51	CD25	5.97E−09	4.19E+05	2.50E−03
1H3-hIgG1-L6-hIL-2 (F42D)	52	CD25	1.04E−08	2.38E+05	2.46E−03
1H3-hIgG1-L6-hIL-2 (F42H)	53	CD25	6.33E−09	4.45E+05	2.81E−03
1H3-hIgG1-L6-hIL-2 (K43A)	54	CD25	1.03E−08	2.85E+05	2.94E−03
1H3-hIgG1-L6-hIL-2 (K43E)	55	CD25	5.47E−09	3.65E+05	2.00E−03
1H3-hIgG1-L6-hIL-2 (K43Q)	56	CD25	4.21E−09	5.14E+05	2.17E−03
1H3-hIgG1-L6-hIL-2 (Y45A)	57	CD25	4.93E−09	4.51E+05	2.22E−03
1H3-hIgG1-L6-hIL-2 (Y45K)	58	CD25	6.56E−09	3.55E+05	2.33E−03
1H3-hIgG1-L6-hIL-2 (Y45S)	59	CD25	6.96E−09	5.07E+05	3.53E−03
1H3-hIgG1-L6-hIL-2 (Y45R)	60	CD25	7.58E−09	4.36E+05	3.31E−03
1H3-hIgG1-L6-hIL-2 (E61A)	61	CD25	1.34E−08	3.13E+05	4.18E−03
1H3-hIgG1-L6-hIL-2 (E61R)	62	CD25	1.30E−08	4.56E+05	5.91E−03
1H3-hIgG1-L6-hIL-2 (E61K)	63	CD25	1.56E−08	3.16E+05	4.94E−03
1H3-hIgG1-L6-hIL-2 (E62A)	64	CD25	1.23E−08	3.79E+05	4.67E−03
1H3-hIgG1-L6-hIL-2 (E62R)	65	CD25	No binding observed		
1H3-hIgG1-L6-hIL-2 (E62K)	66	CD25	No binding observed		
1H3-hIgG1-L6-hIL-2 (E62Y)	67	CD25	1.55E−08	2.91E+05	4.50E−03
1H3-hIgG1-L6-hIL-2 (E68Y)	68	CD25	8.18E−09	1.80E+05	1.47E−03
1H3-hIgG1-L6-hIL-2 (E68A)	69	CD25	4.49E−09	1.45E+05	6.52E−04
1H3-hIgG1-L6-hIL-2 (E68K)	70	CD25	1.05E−08	2.02E+05	2.12E−03
1H3-hIgG1-L6-hIL-2 (E68R)	71	CD25	8.51E−09	2.27E+05	1.93E−03
1H3-hIgG1-L6-hIL-2 (E68L)	72	CD25	2.72E−09	7.79E+04	2.12E−04
1H3-hIgG1-L6-hIL-2 (L72Y)	73	CD25	6.39E−09	1.94E+05	1.24E−03
1H3-hIgG1-L6-hIL-2 (L72R)	74	CD25	1.96E−08	3.07E+04	6.01E−04
1H3-hIgG1-L6-hIL-2 (L72A)	75	CD25	9.08E−09	1.47E+05	1.34E−03
1H3-hIgG1-L6-hIL-2 (L72D)	76	CD25	9.52E−09	1.57E+05	1.50E−03
1H3-hIgG1-L6-hIL-2 (L72H)	77	CD25	9.03E−09	1.65E+05	1.49E−03
1H3-hIgG1-L6-hIL-2 (L72F)	78	CD25	5.04E−09	2.28E+05	1.15E−03
1H3-hIgG1-L6-hIL-2 (R81A)	97	CD122	7.08E−09	2.20E+05	1.56E−03
1H3-hIgG1-L6-hIL-2 (D84A)	98	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (D84R)	99	CD122	1.88E−08	4.73E+05	8.88E−03
1H3-hIgG1-L6-hIL-2 (S87A)	101	CD122	7.09E−09	3.31E+05	2.34E−03

TABLE 3-continued

Binding kinetics of 1H3-hIgG-L6-hIL-2 fusion proteins to recombinant human CD122 by Octet BLI

1H3-hIgG-L6-hIL-2 fusion proteins	SEQ ID NO of hIL-2 variant	Predicted receptor sub-unit targeted by IL-2 substitution	K_D (M)	k_{on} (1/Ms)	k_{off} (1/s)
1H3-hIgG1-L6-hIL-2 (N88Y)	102	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (N88D)	103	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (N88R)	104	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (N88E)	105	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (N88F)	106	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (N88I)	107	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (I92A)	108	CD122	3.38E−09	1.95E+06	6.58E−03
1H3-hIgG1-L6-hIL-2 (I92Y)	109	CD122	1.23E−08	4.53E+05	5.57E−03
1H3-hIgG1-L6-hIL-2 (I92S)	110	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (I92F)	111	CD122	5.45E−09	1.03E+05	5.59E−04
1H3-hIgG1-L6-hIL-2 (I92R)	112	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (I92D)	113	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (I92E)	114	CD122	1.62E−09	9.33E+05	1.51E−03
1H3-hIgG1-L6-hIL-2 (E95A)	115	CD122	8.17E−09	2.87E+05	2.35E−03
1H3-hIgG1-L6-hIL-2 (E95R)	116	CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (E95K)	117	CD122	3.81E−09	6.58E+05	2.51E−03
1H3-hIgG1-L6-hIL-2 (F42K/Y45R/D20A/S87A)	213	CD25 + CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (F42K/Y45R/D20A/E95A)	214	CD25 + CD122	No binding observed		
1H3-hIgG1-L6-hIL-2 (F42K/Y45R/Q126D)	228	CD25 +CD132	9.16E−09	3.75E+05	3.44E−03
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Q126D)	229	CD122 + CD132	No binding observed		
1H3-hIgG1-L6-hIL-2 (R38D/E61R)	79	CD25	1.29E−08	3.68E+05	4.73E−03
1H3-hIgG1-L6-hIL-2 (R38D/E61R/K43E)	80	CD25	7.47E−09	4.52E+05	3.38E−03

[a]SEQ ID NO: 345 corresponds to wild type hIL-2.
[b]SEQ ID NO: 57 is attenuated IL-2 sequence only.

Example 3: Testing for Attenuation for the High-Affinity and Intermediate-Affinity hIL-2 Receptor with a Fixed Concentration Cell-Based Potency pSTAT5 Screen

The attenuation of antibody-attenuated hIL-2 fusion proteins described in Example 2 was tested in a fixed concentration pSTAT5 screen using the NK-92 (expressing the high affinity hIL-2 receptor) and TF1+IL-2Rβ (expressing the intermediate affinity hIL-2 receptor) cell lines as described in Protocol D. Tables 4-8 list the fold change of geometric mean fluorescent intensity (gMFI) of antibody-attenuated hIL-2 fusion proteins from free cytokine wild-type rhIL-2, a measurement of reduction of IL-2 activity. For the fixed concentration screen, the fold change was calculated by dividing the gMFI of the rhIL-2 by the gMFI of the variants. For experiments with full titration curves, fold change from rhIL-2 was calculated by dividing the EC_{50} values for the rhIL-2 by the EC_{50} of variants. Fold change was rounded to the nearest whole number. A reduced gMFI in both NK-92 and TF1+IL-2Rβ cell lines when compared to the gMFI resulting from rhIL-2 was indicative of attenuation of IL-2 activity at both the high- and intermediate-affinity receptors. Group 1 variants described in Example 2 were not tested in the fixed concentration cell-based potency pSTAT5 screen.

Each variant tested was also assessed for IL-2 agonistic activity and characterized either as a full or partial IL-2 agonist, or having no IL-2 activity (inactive). 1H3-hIgG1-L6-hIL-2 fusion protein dose-titration curves that reached the maximal gMFI level exhibited by the rhIL-2 positive control were considered to be antibody-attenuated hIL-2 fusion protein with full agonist activity. Partial agonist activity was calculated as a percentage of full activity using rhIL-2 maximal gMFI as 100%. Antibody-attenuated hIL-2 fusion protein with less than 10% of the rhIL-2 maximal gMFI at the highest concentration of 1200 nM were considered to have no agonist activity (inactive). Some EC_{50} values and level of attenuation could not be accurately calculated using the GraphPad Prism 7 software since activity did not reach a maximum and accordingly these values are an estimate.

pSTAT5 fixed concentration results demonstrated that while some single residue substitutions attenuated IL-2 activity on the high-affinity cell line (NK-92), a combination of substitutions which modulated binding to both the alpha chain and the beta chain or both the alpha chain and gamma chain were required to substantially attenuate IL-2 activity on the high affinity IL-2 receptor (more than 20-fold attenuation from recombinant hIL-2).

TABLE 4

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 2

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (R38D)	47	7	1
1H3-hIgG1-L6-hIL-2 (R38E)	48	12	1
1H3-hIgG1-L6-hIL-2 (R38Q)	49	1	1
1H3-hIgG1-L6-hIL-2 (F42R)	50	7	1
1H3-hIgG1-L6-hIL-2 (F42A)	51	1	1
1H3-hIgG1-L6-hIL-2 (F42H)	53	1	1
1H3-hIgG1-L6-hIL-2 (K43E)	55	1	1
1H3-hIgG1-L6-hIL-2 (K43Q)	56	1	1
1H3-hIgG1-L6-hIL-2 (Y45A)	57	1	1
1H3-hIgG1-L6-hIL-2 (Y45K)	58	1	1
1H3-hIgG1-L6-hIL-2 (Y45S)	59	1	1
1H3-hIgG1-L6-hIL-2 (Y45R)	60	10	1
1H3-hIgG1-L6-hIL-2 (E68Y)	68	1	1
1H3-hIgG1-L6-hIL-2 (E68A)	69	1	1
1H3-hIgG1-L6-hIL-2 (E68L)	72	2	1
1H3-hIgG1-L6-hIL-2 (L72Y)	73	1	1
1H3-hIgG1-L6-hIL-2 (L72A)	75	1	1
1H3-hIgG1-L6-hIL-2 (L72F)	78	1	1
1H3-hIgG1-L6-hIL-2 (R38D/E61R)	79	NT-1	1
1H3-hIgG1-L6-hIL-2 (R38D/E61R/K43E)	80	NT-1	1
1H3-hIgG1-L6-hIL-2 (T3A/F42A/Y45A/L72G/C125A)	81	10	1

NT-1 = Already tested in pSTAT5 full titration first, no data for fixed concentration assay.

TABLE 5

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 3

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (E15A)	82	1	1
1H3-hIgG1-L6-hIL-2 (E15R)	83	1	1
1H3-hIgG1-L6-hIL-2 (E15K)	84	1	1
1H3-hIgG1-L6-hIL-2 (H16A)	85	1	1
1H3-hIgG1-L6-hIL-2 (H16Y)	86	1	1
1H3-hIgG1-L6-hIL-2 (H16E)	87	1	NT-1
1H3-hIgG1-L6-hIL-2 (L19A)	88	1	NT-1
1H3-hIgG1-L6-hIL-2 (D20I)	89	12	NT-1
1H3-hIgG1-L6-hIL-2 (D20S)	90	4	NT-1
1H3-hIgG1-L6-hIL-2 (D20H)	91	10	NT-1
1H3-hIgG1-L6-hIL-2 (D20W)	93	16	NT-1
1H3-hIgG1-L6-hIL-2 (D20Y)	94	17	NT-1
1H3-hIgG1-L6-hIL-2 (D20R)	95	19	NT-1
1H3-hIgG1-L6-hIL-2 (D20F)	96	17	NT-1
1H3-hIgG1-L6-hIL-2 (R81A)	97	1	1
1H3-hIgG1-L6-hIL-2 (D84A)	98	1	NT-1
1H3-hIgG1-L6-hIL-2 (D84R)	99	3	NT-1
1H3-hIgG1-L6-hIL-2 (D84K)	100	2	NT-1
1H3-hIgG1-L6-hIL-2 (S87A)	101	1	1
1H3-hIgG1-L6-hIL-2 (N88Y)	102	22	NT-1
1H3-hIgG1-L6-hIL-2 (N88D)	103	2	NT-1
1H3-hIgG1-L6-hIL-2 (N88R)	104	3	NT-1

TABLE 5-continued

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 3

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (N88E)	105	10	NT-1
1H3-hIgG1-L6-hIL-2 (N88F)	106	19	NT-1
1H3-hIgG1-L6-hIL-2 (N88I)	107	9	NT-1
1H3-hIgG1-L6-hIL-2 (I92A)	108	1	1
1H3-hIgG1-L6-hIL-2 (I92Y)	109	1	NT-1
1H3-hIgG1-L6-hIL-2 (I92S)	110	1	NT-1
1H3-hIgG1-L6-hIL-2 (I92F)	111	1	1
1H3-hIgG1-L6-hIL-2 (I92R)	112	1	NT-1
1H3-hIgG1-L6-hIL-2 (I92D)	113	3	NT-1
1H3-hIgG1-L6-hIL-2 (I92E)	114	1	1
1H3-hIgG1-L6-hIL-2 (E95A)	115	1	1
1H3-hIgG1-L6-hIL-2 (E95R)	116	1	NT-1
1H3-hIgG1-L6-hIL-2 (E95K)	117	1	1
1H3-hIgG1-L6-hIL-2 (D20T)	92	3	2
1H3-hIgG1-L6-hIL-2 (D20A)	31	7	2
1H3-hIgG1-L6-hIL-2 (D20Y/H16E)	118	6	4
1H3-hIgG1-L6-hIL-2 (D20Y/H16A)	119	10	3
1H3-hIgG1-L6-hIL-2 (D20Y/H16Y)	120	10	4
1H3-hIgG1-L6-hIL-2 (D20Y/192A)	121	11	4
1H3-hIgG1-L6-hIL-2 (D20Y/192S)	122	11	4
1H3-hIgG1-L6-hIL-2 (D20Y/192R)	123	12	5
1H3-hIgG1-L6-hIL-2 (D20Y/E95R)	124	12	5
1H3-hIgG1-L6-hIL-2 (D20Y/E95A)	125	11	5

NT-1 = Already tested in pSTAT5 full titration first, no data for fixed concentration assay.

TABLE 6

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 4

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E15A)	82	17	1
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20I)	89	21	15
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20S)	90	2	14
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20H)	91	22	15
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20W)	93	23	15
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20Y)	94	23	16
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20R)	95	23	16
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20F)	96	23	18
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D84K)	100	23	17
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (S87A)	101	17	2
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88Y)	102	23	18
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88D)	103	23	17

TABLE 6-continued

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 4

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88R)	104	24	17
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88E)	105	25	18
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88F)	106	25	18
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88I)	107	25	20

TABLE 6-continued

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 4

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 I192A)	108	15	3
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E95A)	115	14	1
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E95K)	117	25	8

TABLE 7

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 5

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (F42D/D20A)	127	11	3
1H3-hIgG1-L6-hIL-2 (F42R/D20A)	128	10	2
1H3-hIgG1-L6-hIL-2 (F42K/D20A)	129	10	4
1H3-hIgG1-L6-hIL-2 (F42A/D20A)	130	11	3
1H3-hIgG1-L6-hIL-2 (F42H/D20A)	131	12	2
1H3-hIgG1-L6-hIL-2 (Y45R/D20A)	132	11	1
1H3-hIgG1-L6-hIL-2 (Y45K/D20A)	133	11	2
1H3-hIgG1-L6-hIL-2 (R38N/D20A)	134	14	3
1H3-hIgG1-L6-hIL-2 (R38G/D20A)	135	13	2
1H3-hIgG1-L6-hIL-2 (R38H/D20A)	136	12	3
1H3-hIgG1-L6-hIL-2 (R38I/D20A)	137	11	3
1H3-hIgG1-L6-hIL-2 (R38L/D20A)	138	11	4
1H3-hIgG1-L6-hIL-2 (R38M/D20A)	139	11	3
1H3-hIgG1-L6-hIL-2 (R38F/D20A)	140	12	3
1H3-hIgG1-L6-hIL-2 (R38P/D20A)	141	13	3
1H3-hIgG1-L6-hIL-2 (R38S/D20A)	142	15	2
1H3-hIgG1-L6-hIL-2 (R38T/D20A)	143	13	3
1H3-hIgG1-L6-hIL-2 (R38W/D20A)	144	14	2
1H3-hIgG1-L6-hIL-2 (R38Y/D20A)	145	14	3
1H3-hIgG1-L6-hIL-2 (R38V/D20A)	146	12	3
1H3-hIgG1-L6-hIL-2 (R38A/D20A)	147	13	3
1H3-hIgG1-L6-hIL-2 (R38Q/D20A)	148	14	3
1H3-hIgG1-L6-hIL-2 (R38E/D20A)	149	15	3
1H3-hIgG1-L6-hIL-2 (R38D/D20A)	150	15	3
1H3-hIgG1-L6-hIL-2 (K43E/D20A)	151	13	2
1H3-hIgG1-L6-hIL-2 (E61A/D20A)	152	14	2
1H3-hIgG1-L6-hIL-2 (E62A/D20A)	153	14	2
1H3-hIgG1-L6-hIL-2 (E62Y/D20A)	154	14	3
1H3-hIgG1-L6-hIL-2 (L72D/D20A)	155	14	2
1H3-hIgG1-L6-hIL-2 (L72H/D20A)	156	14	3
1H3-hIgG1-L6-hIL-2 (L72R/D20A)	157	10	3
1H3-hIgG1-L6-hIL-2 (F42D/I92D)	158	12	5
1H3-hIgG1-L6-hIL-2 (F42R/I92D)	159	12	3
1H3-hIgG1-L6-hIL-2 (F42H/I92D)	160	12	2
1H3-hIgG1-L6-hIL-2 (F42A/I92D)	161	12	3
1H3-hIgG1-L6-hIL-2 (K43E/I92D)	162	13	4
1H3-hIgG1-L6-hIL-2 (Y45R/I92D)	163	13	1
1H3-hIgG1-L6-hIL-2 (Y45K/I92D)	164	13	1
1H3-hIgG1-L6-hIL-2 (E62A/I92D)	165	13	3
1H3-hIgG1-L6-hIL-2 (E62Y/I92D)	166	14	5
1H3-hIgG1-L6-hIL-2 (L72D/I92D)	167	14	5
1H3-hIgG1-L6-hIL-2 (L72H/I92D)	168	14	5
1H3-hIgG1-L6-hIL-2 (L72R/I92D)	169	14	5
1H3-hIgG1-L6-hIL-2 (R38D/I92D)	170	15	2
1H3-hIgG1-L6-hIL-2 (R38E/I92D)	171	15	2
1H3-hIgG1-L6-hIL-2 (R38Q/I92D)	172	14	2
1H3-hIgG1-L6-hIL-2 (R38A/I92D)	173	13	4
1H3-hIgG1-L6-hIL-2 (R38E/N88R)	174	16	1
1H3-hIgG1-L6-hIL-2 (R38E/D84R)	175	14	2

TABLE 7-continued

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 5

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (R38E/D84K)	176	14	2
1H3-hIgG1-L6-hIL-2 (F42A/Y45R/D20A)	177	11	2
1H3-hIgG1-L6-hIL-2 (F42H/Y45R/D20A)	178	12	2
1H3-hIgG1-L6-hIL-2 (R38D/E61R/D20A)	179	12	3
1H3-hIgG1-L6-hIL-2 (R38E/E61R/D20A)	180	11	3
1H3-hIgG1-L6-hIL-2 (R38Q/E61R/D20A)	181	12	3
1H3-hIgG1-L6-hIL-2 (R38A/E61R/D20A)	182	13	3
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38A)	183	6	5
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38D)	184	21	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38E)	185	21	5
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38Q)	186	19	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42R)	187	21	4
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42A)	188	21	5
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42D)	189	22	12
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42H)	190	22	4
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42K)	191	21	4
1H3-hIgG1-L6-hIL-2 (D20A/E95A/K43A)	192	5	7
1H3-hIgG1-L6-hIL-2 (D20A/E95A/K43E)	193	13	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/K43Q)	194	5	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Y45A)	195	4	5
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Y45K)	196	22	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Y45S)	197	5	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Y45R)	198	25	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E61A)	199	10	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62A)	200	23	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62R)	201	25	17
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62K)	202	25	15
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62Y)	203	25	10
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E68Y)	204	8	5
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E68A)	205	5	8
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E68L)	206	7	9
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72Y)	207	1	5
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72R)	208	12	9
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72A)	209	2	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72D)	210	21	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72H)	211	14	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72F)	212	2	6
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42K/Y45R)	214	21	5
1H3-hIgG1-L6-hIL-2 (D20A/R38E/C125A)	215	16	3
1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E)	216	18	2
1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E/C125A)	217	18	3
1H3-hIgG1-L6-hIL-2 (Δ1-3APT/D20A/R38E)	218	13	1
1H3-hIgG1-L6-hIL-2 (Δ1-3APT/D20A/R38E/C125A)	219	15	4
1H3-hIgG1-L6-hIL-2 (R38E/Q22A)	220	12	0
1H3-hIgG1-L6-hIL-2 (R38E/T123A)	221	12	0
1H3-hIgG1-L6-hIL-2 (R38E/I129A)	222	13	1
1H3-hIgG1-L6-hIL-2 (R38E/S130A)	223	12	0
1H3-hIgG1-L6-hIL-2 (R38E/Q126A)	224	13	1
1H3-hIgG1-L6-hIL-2 (R38E/Q126D)	225	15	4
1H3-hIgG1-L6-hIL-2 (R38E/Q126V)	226	14	1
1H3-hIgG1-L6-hIL-2 (R38E/Q22A/S130A)	227	13	1

TABLE 8

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 6

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (D20A/E61R)	230	25	4
1H3-hIgG1-L6-hIL-2 (D20A/E61N)	231	15	1
1H3-hIgG1-L6-hIL-2 (D20A/E61D)	232	11	0
1H3-hIgG1-L6-hIL-2 (D20A/E61Q)	233	16	2
1H3-hIgG1-L6-hIL-2 (D20A/E61G)	234	15	2
1H3-hIgG1-L6-hIL-2 (D20A/E61H)	235	15	2
1H3-hIgG1-L6-hIL-2 (D20A/E61I)	236	16	1

TABLE 8-continued

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 6

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (D20A/E61L)	237	16	1
1H3-hIgG1-L6-hIL-2 (D20A/E61K)	238	17	2
1H3-hIgG1-L6-hIL-2 (D20A/E61M)	239	15	2
1H3-hIgG1-L6-hIL-2 (D20A/E61F)	240	14	0
1H3-hIgG1-L6-hIL-2 (D20A/E61P)	241	15	1
1H3-hIgG1-L6-hIL-2 (D20A/E61S)	242	16	1
1H3-hIgG1-L6-hIL-2 (D20A/E61T)	243	16	2

TABLE 8-continued

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 6

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (D20A/E61W)	244	15	2
1H3-hIgG1-L6-hIL-2 (D20A/E61Y)	245	15	2
1H3-hIgG1-L6-hIL-2 (D20A/E61V)	246	17	3
1H3-hIgG1-L6-hIL-2 (D20A/F42N)	247	15	2
1H3-hIgG1-L6-hIL-2 (D20A/F42Q)	248	15	2
1H3-hIgG1-L6-hIL-2 (D20A/F42E)	249	16	1
1H3-hIgG1-L6-hIL-2 (D20A/F42G)	250	17	2
1H3-hIgG1-L6-hIL-2 (D20A/F42I)	251	17	2
1H3-hIgG1-L6-hIL-2 (D20A/F42L)	252	14	2
1H3-hIgG1-L6-hIL-2 (D20A/F42M)	253	15	2
1H3-hIgG1-L6-hIL-2 (D20A/F42P)	254	17	2
1H3-hIgG1-L6-hIL-2 (D20A/F42S)	255	15	2
1H3-hIgG1-L6-hIL-2 (D20A/F42T)	256	16	2
1H3-hIgG1-L6-hIL-2 (D20A/F42W)	257	16	2
1H3-hIgG1-L6-hIL-2 (D20A/F42Y)	258	17	2
1H3-hIgG1-L6-hIL-2 (D20A/F42V)	259	18	2
1H3-hIgG1-L6-hIL-2 (D20A/Y45A)	260	15	2
1H3-hIgG1-L6-hIL-2 (D20A/Y45N)	261	14	2
1H3-hIgG1-L6-hIL-2 (D20A/Y45D)	262	18	3
1H3-hIgG1-L6-hIL-2 (D20A/Y45Q)	263	17	3
1H3-hIgG1-L6-hIL-2 (D20A/Y45E)	264	18	3
1H3-hIgG1-L6-hIL-2 (D20A/Y45G)	265	18	2
1H3-hIgG1-L6-hIL-2 (D20A/Y45H)	266	16	2
1H3-hIgG1-L6-hIL-2 (D20A/Y45I)	267	13	2
1H3-hIgG1-L6-hIL-2 (D20A/Y45L)	268	13	2
1H3-hIgG1-L6-hIL-2 (D20A/Y45M)	269	16	3
1H3-hIgG1-L6-hIL-2 (D20A/Y45F)	270	13	2
1H3-hIgG1-L6-hIL-2 (D20A/Y45P)	271	25	4
1H3-hIgG1-L6-hIL-2 (D20A/Y45S)	272	14	3
1H3-hIgG1-L6-hIL-2 (D20A/Y45T)	273	24	3
1H3-hIgG1-L6-hIL-2 (D20A/Y45W)	274	19	3
1H3-hIgG1-L6-hIL-2 (D20A/Y45V)	275	21	3
1H3-hIgG1-L6-hIL-2 (I92D/F42N)	276	29	5
1H3-hIgG1-L6-hIL-2 (I92D/F42Q)	277	29	4
1H3-hIgG1-L6-hIL-2 (I92D/F42E)	278	30	5
1H3-hIgG1-L6-hIL-2 (I92D/F42G)	279	32	5
1H3-hIgG1-L6-hIL-2 (I92D/F42I)	280	31	4
1H3-hIgG1-L6-hIL-2 (I92D/F42L)	281	31	5
1H3-hIgG1-L6-hIL-2 (I92D/F42K)	282	26	4
1H3-hIgG1-L6-hIL-2 (I92D/F42M)	283	28	5
1H3-hIgG1-L6-hIL-2 (I92D/F42P)	284	29	4
1H3-hIgG1-L6-hIL-2 (I92D/F42S)	285	30	5
1H3-hIgG1-L6-hIL-2 (I92D/F42T)	286	28	3
1H3-hIgG1-L6-hIL-2 (I92D/F42W)	287	18	4
1H3-hIgG1-L6-hIL-2 (I92D/F42Y)	288	22	3
1H3-hIgG1-L6-hIL-2 (I92D/F42V)	289	30	3
1H3-hIgG1-L6-hIL-2 (I92D/Y45A)	290	11	3
1H3-hIgG1-L6-hIL-2 (I92D/Y45N)	291	4	3
1H3-hIgG1-L6-hIL-2 (I92D/Y45D)	292	29	5
1H3-hIgG1-L6-hIL-2 (I92D/Y45Q)	293	25	3
1H3-hIgG1-L6-hIL-2 (I92D/Y45E)	294	27	4
1H3-hIgG1-L6-hIL-2 (I92D/Y45G)	295	20	3
1H3-hIgG1-L6-hIL-2 (I92D/Y45H)	296	7	3
1H3-hIgG1-L6-hIL-2 (I92D/Y45I)	297	20	4
1H3-hIgG1-L6-hIL-2 (I92D/Y45L)	298	5	3
1H3-hIgG1-L6-hIL-2 (I92D/Y45M)	299	14	3
1H3-hIgG1-L6-hIL-2 (I92D/Y45F)	300	10	3
1H3-hIgG1-L6-hIL-2 (I92D/Y45P)	301	28	4
1H3-hIgG1-L6-hIL-2 (I92D/Y45S)	302	11	3
1H3-hIgG1-L6-hIL-2 (I92D/Y45T)	303	28	4
1H3-hIgG1-L6-hIL-2 (I92D/Y45W)	304	27	4
1H3-hIgG1-L6-hIL-2 (I92D/Y45V)	305	28	5
1H3-hIgG1-L6-hIL-2 (R38E/D20H)	306	17	5
1H3-hIgG1-L6-hIL-2 (R38E/D20S)	307	17	3
1H3-hIgG1-L6-hIL-2 (F42A/N88R)	308	18	3
1H3-hIgG1-L6-hIL-2 (F42A/N88D)	309	18	3
1H3-hIgG1-L6-hIL-2 (R38E/D84A)	310	18	1
1H3-hIgG1-L6-hIL-2 (R38E/D84N)	311	18	1
1H3-hIgG1-L6-hIL-2 (R38E/D84Q)	312	18	1
1H3-hIgG1-L6-hIL-2 (R38E/D84E)	313	16	1
1H3-hIgG1-L6-hIL-2 (R38E/D84G)	314	18	1
1H3-hIgG1-L6-hIL-2 (R38E/D84H)	315	19	2

TABLE 8-continued

Fold change from rhIL-2 in a fixed concentration pSTAT5 screen on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 6

Variants	SEQ ID NO of hIL-2 variant	Fold change from hIL-2 (NK-92)	Fold change from hIL-2 (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (R38E/D84I)	316	20	1
1H3-hIgG1-L6-hIL-2 (R38E/D84L)	317	19	1
1H3-hIgG1-L6-hIL-2 (R38E/D84M)	318	20	2
1H3-hIgG1-L6-hIL-2 (R38E/D84F)	319	20	2
1H3-hIgG1-L6-hIL-2 (R38E/D84P)	320	20	1
1H3-hIgG1-L6-hIL-2 (R38E/D84S)	321	21	1
1H3-hIgG1-L6-hIL-2 (R38E/D84T)	322	20	1
1H3-hIgG1-L6-hIL-2 (R38E/D84W)	323	21	1
1H3-hIgG1-L6-hIL-2 (R38E/D84Y)	324	21	1
1H3-hIgG1-L6-hIL-2 (R38E/D84V)	325	22	1
1H3-hIgG1-L6-hIL-2 (R38E/I92A)	326	22	1
1H3-hIgG1-L6-hIL-2 (R38E/I92R)	327	22	2
1H3-hIgG1-L6-hIL-2 (R38E/I92N)	328	22	1
1H3-hIgG1-L6-hIL-2 (R38E/I92Q)	329	22	1
1H3-hIgG1-L6-hIL-2 (R38E/I92E)	330	22	2
1H3-hIgG1-L6-hIL-2 (R38E/I92G)	331	22	1
1H3-hIgG1-L6-hIL-2 (R38E/I92H)	332	21	1
1H3-hIgG1-L6-hIL-2 (R38E/I92L)	333	17	1
1H3-hIgG1-L6-hIL-2 (R38E/I92K)	334	24	3
1H3-hIgG1-L6-hIL-2 (R38E/I92M)	335	20	1
1H3-hIgG1-L6-hIL-2 (R38E/I92F)	336	16	1
1H3-hIgG1-L6-hIL-2 (R38E/I92P)	337	24	5
1H3-hIgG1-L6-hIL-2 (R38E/I92S)	338	22	2
1H3-hIgG1-L6-hIL-2 (R38E/I92T)	339	22	1
1H3-hIgG1-L6-hIL-2 (R38E/I92W)	340	23	1
1H3-hIgG1-L6-hIL-2 (R38E/I92Y)	341	21	1
1H3-hIgG1-L6-hIL-2 (R38E/I92V)	342	21	1
1H3-hIgG1-L6-hIL-2 (R38E/H16E)	343	25	3
1H3-hIgG1-L6-hIL-2 (R38K/D20A)	344	17	3

Example 4: Testing for Attenuation of IL-2 Fusion Proteins for Each of the High-Affinity and Intermediate-Affinity hIL-2 Receptors with a Cell-Based Potency pSTAT5 Dose-Titration Screen

The attenuation of selected antibody-attenuated hIL-2 fusion proteins described in Example 2 (1H3-hIgG1-L6-hIL-2 fusion protein from Groups 2-6) were tested in pSTAT5 titration curves using the NK-92 and TF1+IL-2Rβ cell lines as described in Protocol D.

The gMFI of the Alexa Fluor 647 pSTAT5-positive signal was used to generate four parameter logistic curves and GraphPad Prism 7 software was then used to calculate EC_{50} values. These values were compared to recombinant hIL-2 (rhIL-2) control as a measurement of attenuation. Tables 9-13 summarize the fold change in activity from rhIL-2 calculated using the gMFI of the Alexa Fluor 647 signal.

An increase in the fold change from rhIL-2 was indicative of the degree of attenuation of hIL-2 activity. Each antibody-attenuated hIL-2 fusion protein tested in the pSTAT5 titration curve was also assessed for agonistic activity and characterized as either full, partial, or no activity (inactive). Antibody-attenuated hIL-2 fusion protein dose-titration curves that reached the maximal gMFI level as the rhIL-2 were considered to be variants with full agonist activity. Partial agonist activity was calculated as described in Example 3. Inactive antibody-attenuated hIL-2 fusion proteins were classified as having less than 10% activity in comparison to rhIL-2. Some fold changes from rhIL-2 could not be accurately calculated (denoted as Not Calculated or "NC") using the GraphPad Prism 7 software since a full four parameter logistic curve was not generated and accordingly these values are an estimate (annotated as [a] in Tables 9-13).

However, these variants had greater than 10,000-fold attenuation from rhIL-2 on graphs (data not shown). This is denoted on Tables 9-13 as ">10,000 on graph; NC"

Full titration pSTAT5 curves demonstrated similar findings as presented in Example 3 in which substitutions that modulated binding to both the alpha chain and the beta chain substantially attenuated IL-2 activity on the high affinity IL-2 receptor in comparison to single substitutions for binding to the alpha or beta chain only. The full titration pSTAT5 assay was additionally able to differentiate between variants with substitutions that caused inactivity versus highly attenuated variants. Finally, comparison of dose-titration curves illustrated more accurate of levels of attenuation over a fixed concentration assay.

TABLE 9

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 2

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (R38A)	46	2	Full	0	Full
1H3-hIgG1-L6-hIL-2 (R38D)	47	55	Full	1	Full
1H3-hIgG1-L6-hIL-2 (R38E)	48	99-136	Full	0	Full
1H3-hIgG1-L6-hIL-2 (F42R)	50	65	Full	0	Full
1H3-hIgG1-L6-hIL-2 (F42D)	52	193	Full	0	Full
1H3-hIgG1-L6-hIL-2 (K43A)	54	3 [a]	Full	0	Full
1H3-hIgG1-L6-hIL-2 (Y45R)	57	81 [a]	Full	0	Full
1H3-hIgG1-L6-hIL-2 (E61A)	61	3 [a]	Full	0	Full
1H3-hIgG1-L6-hIL-2 (E61R)	62	22 [a]	Full	0	Full
1H3-hIgG1-L6-hIL-2 (E61K)	63	14 [a]	Full	0	Full
1H3-hIgG1-L6-hIL-2 (E62A)	64	6 [a]	Full	0	Full
1H3-hIgG1-L6-hIL-2 (E62R)	65	>10,000	Partial, 80%	38	Full
1H3-hIgG1-L6-hIL-2 (E62K)	66	2048	Full	10	Full
1H3-hIgG1-L6-hIL-2 (E62Y)	67	18	Full	0	Full
1H3-hIgG1-L6-hIL-2 (E68K)	70	2 [a]	Full	0	Full
1H3-hIgG1-L6-hIL-2 (E68R)	71	3 [a]	Full	0	Full
1H3-hIgG1-L6-hIL-2 (L72R)	74	2 [a]	Full	1	Full
1H3-hIgG1-L6-hIL-2 (L72D)	76	4 [a]	Full	0	Full
1H3-hIgG1-L6-hIL-2 (L72H)	77	1 [a]	Partial, 80%	0	Full
1H3-hIgG1-L6-hIL-2 (R38D/E61R)	79	479	Partial, 80%	NT	NT
1H3-hIgG1-L6-hIL-2 (R38D/E61R/K43E)	80	598	Full	NT	NT
1H3-hIgG1-L6-hIL-2 (T3A/F42A/Y45A/L72G/C125A)	81	360-1426	Full	0	Full

NT = not tested

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

TABLE 10

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins variants from Group 3

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (H16E)	87	63	Full	63	Full
1H3-hIgG1-L6-hIL-2 (L19A)	88	0	Full	0	Full
1H3-hIgG1-L6-hIL-2 (D20I)	89	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (D20S)	90	28	Partial, 80%	277 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20H)	91	>10,000 [a]	Partial, 90%	2767 [a]	Partial, 50%
1H3-hIgG1-L6-hIL-2 (D20W)	93	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (D20Y)	94	>10,000 [a]	Partial, 50-70%	84-143 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20R)	95	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (D20F)	96	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (D84A)	98	NT	NT	14	Full
1H3-hIgG1-L6-hIL-2 (D84R)	99	16	Full	244 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D84K)	100	14	Partial, 90%	195 [a]	Full
1H3-hIgG1-L6-hIL-2 (N88Y)	102	NT	NT	>10,000 on graph, NC [a]	Inactive

TABLE 10-continued

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins variants from Group 3

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (N88D)	103	21	Partial, 90%	130	Full
1H3-hIgG1-L6-hIL-2 (N88R)	104	5-27	Partial, 80%-Full	289-556	Partial, 40%
1H3-hIgG1-L6-hIL-2 (N88E)	105	NT	NT	>10,000 on graph, NC [a]	Partial, 40%
1H3-hIgG1-L6-hIL-2 (N88F)	106	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (N88I)	107	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (I92Y)	109	NT	NT	1	Full
1H3-hIgG1-L6-hIL-2 (I92S)	110	NT	NT	8	Full
1H3-hIgG1-L6-hIL-2 (I92R)	112	NT	NT	31	Full
1H3-hIgG1-L6-hIL-2 (I92D)	113	8-20	Full	68-365 [a]	Partial, 70-90%
1H3-hIgG1-L6-hIL-2 (E95R)	116	NT	NT	5	Full
1H3-hIgG1-L6-hIL-2 (D20T)	92	8	Full	167 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A)	31	21	Partial, 80%	117 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20Y/H16E)	94	52 [a]	Partial, 80%	2159 [a]	Partial, 30%
1H3-hIgG1-L6-hIL-2 (D20Y/H16A)	119	>10,000 [a]	Partial, 40%	30 [a]	Partial, 20%
1H3-hIgG1-L6-hIL-2 (D20Y/H16Y)	120	>10,000 [a]	Partial, 40%	343 [a]	Partial, 20%
1H3-hIgG1-L6-hIL-2 (D20Y/I92A)	121	>10,000 [a]	Partial, 20%	4 [a]	Partial, 10%
1H3-hIgG1-L6-hIL-2 (D20Y/I92S)	122	>10,000 [a]	Partial, 10%	12 [a]	Partial, 10%

NT = Not Tested; NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

TABLE 11

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 4

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E15A)	82	184	Full	20	Full
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20I)	89	>10,000 [a]	Partial, 80%	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20S)	90	2403	Full	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20H)	91	>10,000 [a]	Partial, 80%	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20W)	93	>10,000 [a]	Partial, 60%	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20Y)	94	>10,000 [a]	Partial, 90%	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20R)	95	>10,000 [a]	Partial, 80%	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20F)	96	>10,000 [a]	Partial, 70%	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D84K)	100	>10,000	Full	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (S87A)	101	305	Full	44	Full
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88Y)	102	>10,000 [a]	Partial, 50%	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88D)	103	393	Full	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88R)	104	274	Full	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88E)	105	>10,000 [a]	Full	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88F)	106	>10,000 [a]	Partial, 80%	>10,000 on graph, NC [a]	Inactive

TABLE 11-continued

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 4

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88I)	107	7780	Full	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (I92A)	108	26	Full	95	Full
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E95A)	115	30	Full	16	Full
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E95K)	117	792	Full	434 [a]	Partial, 60%

NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

TABLE 12

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 5

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (F42K/D20A)	129	>10,000 [a]	Partial, 30%	219 [a]	Partial, 50%
1H3-hIgG1-L6-hIL-2 (F42A/D20A)	130	>10,000 [a]	Partial, 70%	96 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (R38N/D20A)	134	4497	Partial, 70%	121 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (R38G/D20A)	135	2811	Partial, 70%	139 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (R38H/D20A)	136	1752	Partial, 80%	107 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (R38I/D20A)	137	658	Partial, 70%	107 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (R38L/D20A)	138	532	Partial, 80%	125 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (R38M/D20A)	139	786	Partial, 90%	85 [a]	Partial, 90%
1H3-hIgG1-L6-hIL-2 (R38F/D20A)	140	1072	Partial, 80%	124 [a]	Partial, 90%
1H3-hIgG1-L6-hIL-2 (R38P/D20A)	142	337	Partial, 70%	337 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (R38S/D20A)	142	571	Partial, 70%	571 [a]	Partial, 90%
1H3-hIgG1-L6-hIL-2 (R38V/D20A)	146	765	Partial, 70%	765 [a]	Partial, 90%
1H3-hIgG1-L6-hIL-2 (R38A/D20A)	147	619	Partial, 80%	70 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (R38Q/D20A)	148	4700	Partial, 80%	91 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/R38E)	149	>10,000 [a]	Partial, 60%-Full	409 [a]	Partial, 50%
1H3-hIgG1-L6-hIL-2 (R38D/D20A)	150	>10,000 [a]	Partial, 70%	172 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (K43E/D20A)	151	584	Partial, 90%	231 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (F42R/I92D)	159	801 [a]	Partial, 40%	52 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (F42H/I92D)	160	194	Full	801 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (F42A/I92D)	161	338 [a]	Partial, 70%	194 [a]	Full
1H3-hIgG1-L6-hIL-2 (R38D/I92D)	170	>10,000 [a]	Partial, 80%	338 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (R38E/I92D)	171	>10,000 [a]	Partial, 70%	51 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (R38Q/I92D)	172	561	Full	48 [a]	Partial, 90%
1H3-hIgG1-L6-hIL-2 (R38E/D84R)	175	>10,000 [a]	Partial, 60%	50 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (R38E/D84K)	176	>10,000 [a]	Partial, 40%	45 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (R38D/E61R/D20A)	179	>10,000 on graph, NC [a]	Partial, 40%	62 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (R38E/E61R/D20A)	180	>10,000 [a]	Partial, 90%	181 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (R38Q/E61R/D20A)	181	>10,000 [a]	Partial, 40%	115 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (R38A/E61R/D20A)	182	>10,000 [a]	Partial, 40%	130 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38A)	183	149-199	Partial, 70-80%	157 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38D)	184	>10,000	Partial, 60-70%	84-508 [a]	Full
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38E)	185	>10,000 [a]	Partial, 70-90%	188-427 [a]	Partial, 70%-Full
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38Q)	186	3725	Partial, 70%	124-413 [a]	Partial, 80%-Full
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42R)	187	>10,000 [a]	Partial, 70%	87 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42A)	188	3000-5718 [a]	Partial, 90%	45-244 [a]	Partial, 70%-Full
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42D)	189	>10,000 [a]	Partial, 10%	1451 [a]	Partial, 30%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42H)	190	3579	Partial, 80%	411 [a]	Full
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42K)	191	>10,000 [a]	Partial, 50%	82 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/K43E)	193	386-553	Partial, 80-90%	46-142 [a]	Partial, 50-0%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Y45A)	195	62	Partial, 90%	300 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Y45K)	196	7951 [a]	Partial, 70%	205 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Y45R)	198	>10,000 [a]	Partial, 80%	293 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E61A)	199	367	Partial, 80%	195 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62A)	200	3265 [a]	Partial, 70%	230 [a]	Partial, 50%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62R)	201	>10,000 [a]	Inactive, 5%	>10,000 on graph, NC [a]	Partial, 10%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62K)	202	>10,000 [a]	Inactive, 10%	>10,000 on graph, NC [a]	Partial, 10%

TABLE 12-continued

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 5

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62Y)	203	>10,000 [a]	Partial, 70%	265 [a]	Partial, 40%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E68Y)	204	131	Partial, 80%	61 [a]	Partial, 50%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E68A)	205	45	Partial, 60%	620 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E68L)	206	187	Partial, 80%	172 [a]	Partial, 40%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72R)	208	1178	Full	499 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72D)	210	>10,000 [a]	Partial, 70%	456-504 [a]	Partial, 60-70%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72H)	211	798	Partial, 70%	117 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42K/Y45R)	214	>10,000 [a]	Partial, 60-70%	155 185 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (F42K/Y45R/D20A/S87A)	213	840 [a]	Partial, 70%	155 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/R38E/C125A)	215	>10,000 on graph, NC [a]	Partial, 50%	183-584 [a]	Partial, 50-70%
hIgG1-L6-hIL-2(T3A/D20A/R38E)	216	>10,000 [a]	Partial, 60-90%	77-484 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E/C125A)	217	>10,000 [a]	Partial, 90%	218-512 [a]	Partial, 50-60%
1H3-hIgG1-L6-hIL-2(A1-3APT/D20A/R38E)	218	24-69	Full	6	Full
1H3-hIgG1-L6-hIL-2 (A1-3APT/D20A/R38E/C125A)	219	49-619	Partial, 30-70%	165-619 [a]	Partial, 40-50%
1H3-hIgG1-L6-hIL-2 (R38E/Q126D)	225	>10,000 on graph, NC [a]	Partial, 60%	>10,000 on graph, NC [a]	Partial, 40%
1H3-hIgG1-L6-hIL-2 (F42K/Y45R/Q126D)	228	>10,000 [a]	Partial, 60%	226 [a]	Partial, 50%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Q126D)	229	>10,000 on graph, NC [a]	Inactive	>10,000 on graph, NC [a]	Inactive

NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

TABLE 13

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 6

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (D20A/F42N)	247	>10,000 [a]	Partial, 60%	>10,000 on graph, NC [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/F42Q)	248	>10,000 [a]	Partial, 50%	16 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/F42P)	254	>10,000 [a]	Partial, 60%	13 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/F42S)	255	>10,000 [a]	Partial, 60%	17 [a]	Partial, 40%
1H3-hIgG1-L6-hIL-2 (D20A/Y45E)	264	4717	Partial, 80%	32 [a]	Partial, 50%
1H3-hIgG1-L6-hIL-2 (I92D/F42Q)	277	>10,000 [a]	Partial, 50%	24 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (I92D/F42I)	280	>10,000 [a]	Partial, 30%	117 [a]	Partial, 20%
1H3-hIgG1-L6-hIL-2 (I92D/F42K)	282	>10,000 [a]	Partial, 50%	58 [a]	Partial, 90%
1H3-hIgG1-L6-hIL-2 (I92D/F42T)	286	>10,000 [a]	Partial, 60%	>10,000 on graph, NC [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (R38E/D20S)	307	>10,000 [a]	Partial, 50%	25 [a]	Partial, 40%
1H3-hIgG1-L6-hIL-2 (F42A/N88R)	308	>10,000 [a]	Partial, 70%	34 [a]	Partial, 30%

NC = Not Calculated by GraphPad Prism

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

Example 5: Testing for Attenuation for the High-Affinity and Intermediate-Affinity hIL-2 Receptor with Cell-Based Proliferation Assays

The attenuation of IL-2 activity of antibody-attenuated hIL-2 fusion proteins from Groups 1-6 in Example 2 (2D12-mIgG1-D265A-L6-hIL-2, 2D12-hIgG1-L6-hIL-2, and 1H3-hIgG1-L6-hIL-2 fusion proteins) were tested in proliferation assays in both the NK-92 and TF1+IL-2Rβ cell lines as described in Protocol E. The results of the assays are provided in Tables 14-19.

Selected 1H3-hIgG1-L6-hIL-2 fusion proteins with substantial attenuation in the pSTAT5 titration curves from Example 4 were tested in this cell-based proliferation assay.

pSTAT5 is a downstream read-out of IL-2 activity and assays require only 10 minutes of stimulation which may be a small snapshot of IL-2 dependent activity. For proliferation assays, cells were incubated with 2D12-mIgG1-D265A-L6-hIL-2, 2D12-hIgG1-L6-hIL-2, 1H3-hIgG1-L6-hIL-2 fusion proteins, or recombinant hIL-2 control for 3-4 days, providing a more physiological relevant read-out of IL-2 dependent activity in vivo. Other 2D12-mIgG1-D265A-L6-hIL-2 and 2D12-hIgG1-L6-hIL-2 fusion proteins that were generated but not tested in a pSTAT5 assay were assayed for IL-2 dependent activity using this proliferation assay.

Similar to cell-based pSTAT5 dose-titration experiments, the calculated EC_{50} as determined from relative luminescence units (RLU) instead of gMFI and analysis of the results were performed identically to Example 4 once EC_{50} was calculated. Similar to results identified in Example 4, proliferation curves demonstrated that some substitutions that modulated binding to both the alpha chain and beta chain substantially attenuated IL-2 activity on the high affinity receptor in comparison to single substitutions for binding to the alpha or beta chain only. These selected 1H3-hIgG1-L6-hIL-2 fusion proteins were also tested for proliferation on the TF1+IL-2Rβ cell line and demonstrated that some of these same substitutions substantially attenuated IL-2 activity on the intermediate affinity receptor.

TABLE 14

Fold change from rhIL-2 and agonistic activity on 2D12-mIgG1-D265A-L6-hIL-2 or 2D12-hIgG1-L6-hIL-2 fusion proteins from Group 1 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
2D12-mIgG1-D265A-L6-hIL-2 (F42K)	1	2	Full	0	Full
2D12-mIgG1-D265A-L6-hIL-2 (Y45R)	60	3	Full	2	Full
2D12-hIgG1-L6-hIL-2 (V69A)	2	0	Full	0	Full
2D12-hIgG1-L6-hIL-2 (V69E)	3	13	Partial, 60%	83	Full
2D12-hIgG1-L6-hIL-2 (V69H)	6	41	Partial, 60%	544	Full
2D12-hIgG1-L6-hIL-2 (V69K)	8	>10,000 on graph, NC [a]	Inactive	3033	Partial, 40%
2D12-hIgG1-L6-hIL-2 (V69L)	9	1	Full	1	Full
2D12-hIgG1-L6-hIL-2 (V69F)	4	0	Full	1	Full
2D12-hIgG1-L6-hIL-2 (V69G)	5	108	Full	396	Full
2D12-hIgG1-L6-hIL-2 (V69I)	7	1	Full	1	Full
2D12-hIgG1-L6-hIL-2 (V69M)	10	2	Full	3	Full
2D12-hIgG1-L6-hIL-2 (V69Q)	11	7	Full	16	Full
2D12-mIgG1-D265A-L6-hIL-2 (V69R)	581	2392	Partial, 70%	2973	Partial, 50%
2D12-hIgG1-L6-hIL-2 (V69S)	12	6	Full	13	Full
2D12-hIgG1-L6-hIL-2 (V69T)	13	3	Full	3	Full
2D12-hIgG1-L6-hIL-2 (V69W)	14	0	Full	1	Full
2D12-hIgG1-L6-hIL-2 (V69Y)	15	1	Full	1	Full
2D12-mIgG1-D265A-L6-hIL-2 (D20A)	31	1	Full	>10,000 [a]	Full
2D12-mIgG1-D265A-L6-hIL-2 (D20N)	32	0	Full	>10,000 [a]	Full
2D12-mIgG1-D265A-L6-hIL-2 (D20K)	33	4	Full	>10,000 on graph, NC [a]	Inactive
2D12-mIgG1-D265A-L6-hIL-2 (N88A)	34	0	Full	2289	Full
2D12-mIgG1-D265A-L6-hIL-2 (N88G)	35	0	Full	2978	Full
2D12-mIgG1-D265A-L6-hIL-2 (N88H)	36	1-3	Full	>10,000 on graph, NC [a]	Inactive
2D12-mIgG1-D265A-L6-hIL-2 (N88K)	37	564-9557	Partial, 40%	>10,000 on graph, NC [a]	Inactive
2D12-mIgG1-D265A-L6-hIL-2 (Q126L)	375	0-12	Full	118	Full
2D12-mIgG1-D265A-L6-hIL-2 (Q126E)	376	0-3	Full	40	Full
2D12-mIgG1-D265A-L6-hIL-2 (F42K/F44K)	16	44	Full	>10,000 on graph, NC [a]	Inactive
2D12-mIgG1-D265A-L6-hIL-2 (F42K/Y45R)	17	1-2	Full	0-3	Full
2D12-mIgG1-D265A-L6-hIL-2 (F42K/V69R)	18	1500	Partial, 80%	841	Partial, 80%
2D12-mIgG1-D265A-L6-hIL-2 (Y45R/V69R)	19	1	Full	3	Full
2D12-mIgG1-D265A-L6-hIL-2 (D20A/D84A)	38	1	Full	>10,000 on graph, NC [a]	Inactive
2D12-mIgG1-D265A-L6-hIL-2 (D20A/E15A)	39	0	Full	>10,000 on graph, NC [a]	Partial, 40%
2D12-mIgG1-D265A-L6-hIL-2 (D20A/E95A)	40	0	Full	>10,000 [a]	Full
2D12-mIgG1-D265A-L6-hIL-2 (D20A/N88A)	41	6	Partial, 60%	>10,000 on graph, NC [a]	Inactive
2D12-mIgG1-D265A-L6-hIL-2 (D20A/S87A)	42	0	Full	>10,000 [a]	Full
2D12-mIgG1-D265A-L6-hIL-2 (D84A/N88A)	43	0	Full	>10,000 on graph, NC [a]	Inactive
2D12-mIgG1-D265A-L6-hIL-2 (E15A/N88A)	44	0	Full	4201	Partial, 80%

TABLE 14-continued

Fold change from rhIL-2 and agonistic activity on 2D12-mIgG1-D265A-L6-hIL-2 or 2D12-hIgG1-L6-hIL-2 fusion proteins from Group 1 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
2D12-mIgG1-D265A-L6-hIL-2 (S87A/N88A)	45	0	Full	1521	Full
2D12-mIgG1-D265A-L6-hIL-2 (F42K/F44K/Y45R)	20	NT	NT	0	Full
2D12-mIgG1-D265A-L6-hIL-2 (F42A/Y45A/L72G)	574	0-1	Full	0-3	Full
2D12-mIgG1-D265A-L6-hIL-2 (R38A/F42K/Y45R)	21	1	Full	0	Full
2D12-mIgG1-D265A-L6-hIL-2 (R38E/F42K/Y45R)	22	1-3	Full	0	Full
2D12-mIgG1-D265A-L6-hIL-2 (K43E/F42K/Y45R)	23	0	Full	3	Full
2D12-mIgG1-D265A-L6-hIL-2 (K43T/F42K/Y45R)	24	0	Full	3	Full
2D12-mIgG1-D265A-L6-hIL-2 (F42K/Y45R/E62A)	25	1	Full	0-3	Full
2D12-mIgG1-D265A-L6-hIL-2 (P65R/F42K/Y45R)	26	1	Full	0-2	Full
2D12-mIgG1-D265A-L6-hIL-2 (P65S/F42K/Y45R)	27	1	Full	0-2	Full
2D12-mIgG1-D265A-L6-hIL-2 (V69A/F42K/Y45R)	28	1	Full	0-4	Full
2D12-mIgG1-D265A-L6-hIL-2 (V69D/F42K/Y45R)	29	1	Full	0-5	Full
2D12-mIgG1-D265A-L6-hIL-2 (V69R/F42K/Y45R)	30	1-4	Full	0-6	Full

NT = Not Tested

NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

TABLE 15

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 2 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1+ IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (R38A)	46	0	Full	1	Full
1H3-hIgG1-L6-hIL-2 (R38D)	47	3	Full	0	Full
1H3-hIgG1-L6-hIL-2 (R38E)	48	7	Full	1 [a]	Full
1H3-hIgG1-L6-hIL-2 (F42R)	50	6	Full	0 [a]	Full
1H3-hIgG1-L6-hIL-2 (F42D)	52	10	Full	2	Full
1H3-hIgG1-L6-hIL-2 (K43A)	54	1 [a]	Full	2	Full
1H3-hIgG1-L6-hIL-2 (Y45R)	60	4	Full	0 [a]	Full
1H3-hIgG1-L6-hIL-2 (E61A)	61	0 [a]	Full	1	Full
1H3-hIgG1-L6-hIL-2 (E61R)	62	1	Full	1	Full
1H3-hIgG1-L6-hIL-2 (E61K)	63	1	Full	1	Full
1H3-hIgG1-L6-hIL-2 (E62A)	64	1	Full	1	Full
1H3-hIgG1-L6-hIL-2 (E62R)	65	>10,000 on graph, NC [a]	Inactive	209	Partial, 60%
1H3-hIgG1-L6-hIL-2 (E62K)	66	>10,000 [a]	Partial, 40-70%	67-99	Partial, 60%
1H3-hIgG1-L6-hIL-2 (E62Y)	67	1	Full	1	Full
1H3-hIgG1-L6-hIL-2 (E68K)	70	0	Full	1	Full
1H3-hIgG1-L6-hIL-2 (E68R)	71	1	Full	1	Full
1H3-hIgG1-L6-hIL-2 (L72R)	74	3	Full	3	Full
1H3-hIgG1-L6-hIL-2 (L72D)	76	2	Full	0	Full
1H3-hIgG1-L6-hIL-2 (L72H)	77	1	Full	1	Full
1H3-hIgG1-L6-hIL-2 (R38D/E61R)	79	36	Full	2	Full
1H3-hIgG1-L6-hIL-2 (R38D/E61R/K43E)	80	27	Full	1	Full

TABLE 15-continued

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 2 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1+ IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (T3A/F42A/Y45A/L72G/C125A)	81	142	Full	1-2	Partial, 40%-Full

NT = Not Tested

NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

TABLE 16

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 3 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1+ IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (H16E)	87	0	Full	34	Full
1H3-hIgG1-L6-hIL-2 (L19A)	88	NT	NT	1	Full
1H3-hIgG1-L6-hIL-2 (D20I)	89	NT	NT	8 [a]	Partial, 50%
1H3-hIgG1-L6-hIL-2 (D20S)	90	1	Full	201-304	Partial, 80%-Full
1H3-hIgG1-L6-hIL-2 (D20H)	91	239	Full	986-6461 [a]	Partial, 50-70%
1H3-hIgG1-L6-hIL-2 (D20W)	93	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (D20Y)	94	880-2097 [a]	Full	383	Full
1H3-hIgG1-L6-hIL-2 (D20R)	95	NT	NT	262-275	Full
1H3-hIgG1-L6-hIL-2 (D20F)	96	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (D84A)	98	NT	NT	21	Full
1H3-hIgG1-L6-hIL-2 (D84R)	99	9	Full	269-455	Partial, 80-90%
1H3-hIgG1-L6-hIL-2 (D84K)	100	4	Full	354-385	Partial, 70%-Full
1H3-hIgG1-L6-hIL-2 (N88Y)	102	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (N88D)	103	0	Full	115-137	Partial, 70%-Full
1H3-hIgG1-L6-hIL-2 (N88R)	104	1-5	Partial, 80%-Full	959	Partial, 80%
1H3-hIgG1-L6-hIL-2 (N88E)	105	NT	NT	1162	Partial, 50%
1H3-hIgG1-L6-hIL-2 (N88F)	106	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (N88I)	107	NT	NT	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (I92Y)	109	NT	NT	1	Full
1H3-hIgG1-L6-hIL-2 (I92S)	110	NT	NT	10	Full
1H3-hIgG1-L6-hIL-2 (I92R)	112	NT	NT	13	Full
1H3-hIgG1-L6-hIL-2 (I92D)	113	15-20	Full	609-1006	Partial, 90%-Full
1H3-hIgG1-L6-hIL-2 (E95R)	116	NT	NT	8	Full
1H3-hIgG1-L6-hIL-2 (D20T)	92	2	Full	124-149	Full
1H3-hIgG1-L6-hIL-2 (D20Y/H16E)	118	5	Full	8076 [a]	Partial, 80%

NT = Not Tested

NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

TABLE 17

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 4 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E15A)	82	14	Partial, 90%	13	Partial, 70%

TABLE 17-continued

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 4 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20S)	90	127	Full	8709 [a]	Partial, 50%
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20W)	93	>10,000 on graph, NC [a]	Inactive	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20Y)	94	>10,000 on graph, NC [a]	Partial, 50%	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D84K)	100	783	Partial, 90%	2051 [a]	Partial, 30%
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (S87A)	101	19	Partial, 90%	20	Partial, 90%
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88D)	103	50	Full	3284 [a]	Partial, 90%
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88R)	104	42	Full	6864 [a]	Partial, 50%
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E95K)	117	51	Full	164	Partial, 80%

NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

TABLE 18

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 5 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (F42K/D20A)	129	>10,000 on graph, NC [a]	Partial, 20%	3060 [a]	Full
1H3-hIgG1-L6-hIL-2 (F42A/D20A)	130	>10,000 on graph, NC [a]	Full	2081 [a]	Full
1H3-hIgG1-L6-hIL-2 (R38P/D20A)	141	86	Full	761	Full
1H3-hIgG1-L6-hIL-2 (R38S/D20A)	142	140	Full	662	Full
1H3-hIgG1-L6-hIL-2 (R38V/D20A)	146	11	Full	843	Full
1H3-hIgG1-L6-hIL-2 (D20A/R38E)	149	1183-2016	Partial, 70%-Full	>10,000 [a]	Partial, 80%-Full
1H3-hIgG1-L6-hIL-2 (R38D/D20A)	150	2262 [a]	Full	680	Full
1H3-hIgG1-L6-hIL-2 (F42R/I92D)	159	>10,000 on graph, NC [a]	Partial, 30%	1210	Full
1H3-hIgG1-L6-hIL-2 (F42H/I92D)	160	288 [a]	Full	242 [a]	Full
1H3-hIgG1-L6-hIL-2 (F42A/I92D)	161	>10,000 on graph, NC [a]	Partial, 60%	2275	Partial, 80%
1H3-hIgG1-L6-hIL-2 (R38D/I92D)	170	746 [a]	Partial, 90%	172	Full
1H3-hIgG1-L6-hIL-2 (R38E/I92D)	171	1611 [a]	Full	116	Full
1H3-hIgG1-L6-hIL-2 (R38E/D84R)	175	>10,000 on graph, NC [a]	Full	147	Full
1H3-hIgG1-L6-hIL-2 (R38E/D84K)	176	>10,000 on graph, NC [a]	Partial, 70%	315	Full
1H3-hIgG1-L6-hIL-2 (R38D/E61R/D20A)	179	>10,000 on graph, NC [a]	Partial, 50%	984	Full
1H3-hIgG1-L6-hIL-2 (R38E/E61R/D20A)	180	>10,000 on graph, NC [a]	Full	417	Full
1H3-hIgG1-L6-hIL-2 (R38Q/E61R/D20A)	181	>10,000 on graph, NC [a]	Partial, 80%	803	Full
1H3-hIgG1-L6-hIL-2 (R38A/E61R/D20A)	182	>10,000 on graph, NC [a]	Partial, 60%	1031	Full
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38A)	183	42	Partial, 70%	537	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38D)	184	5315 [a]	Partial, 50%	492	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38E)	185	>10,000 on graph, NC [a]	Full	439	Partial, 90%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/R38Q)	186	572	Full	859	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42R)	187	2096	Partial, 70%	356	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42A)	188	369	Partial, 70%	73	Partial, 90%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42D)	189	>10,000 on graph, NC [a]	Inactive	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42H)	190	641	Partial, 90%	320	Full
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42K)	191	>10,000 on graph, NC [a]	Inactive	272	Partial, 80%

TABLE 18-continued

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 5 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (D20A/E95A/K43E)	193	80	Partial, 90%	1876 [a]	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Y45A)	195	25	Full	82	Partial, 90%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Y45K)	196	>10,000 on graph, NC [a]	Partial, 20%	383	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Y45R)	198	>10,000 on graph, NC [a]	Inactive	57	Partial, 50%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E61A)	199	306 [a]	Partial, 80%	702	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62A)	200	>10,000 on graph, NC [a]	Partial, 20%	661	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62R)	201	>10,000 on graph, NC [a]	Inactive	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62K)	202	>10,000 on graph, NC [a]	Inactive	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E62Y)	203	721	Partial, 40%	982 [a]	Partial, 30%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E68Y)	204	11	Full	469	Full
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E68A)	205	6	Partial, 50%	535	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/E68L)	206	15	Full	972	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72R)	208	655 [a]	Partial, 50%	316	Partial, 40%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72D)	210	5415	Inactive	125	Partial, 90%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/L72H)	211	583 [a]	Partial, 60%	135	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/F42K/Y45R)	214	>10,000 on graph, NC [a]	Inactive	58-209	Partial, 40-80%
1H3-hIgG1-L6-hIL-2 (F42K/Y45R/D20A/S87A)	213	123	Full	0	Full
1H3-hIgG1-L6-hIL-2 (D20A/R38E/C125A)	215	>10,000 [a]	Partial, 30-90%	2102 [a]	Partial, 80%
1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E)	216	2338-5870	Partial, 80%-Full	353-571	Full
1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E/C125A)	217	>10,000 [a]	Full	1086 [a]	Partial, 80%-Full
1H3-hIgG1-L6-hIL-2 (Δ1-3APT/D20A/R38E)	218	4-16	Full	32	Partial, 90%
1H3-hIgG1-L6-hIL-2 (Δ1-3APT/D20A/R38E/C125A)	219	>10,000 [a]	Inactive-Partial, 50%	993 [a]	Partial, 60%
1H3-hIgG1-L6-hIL-2 (F42K/Y45R/Q126D)	228	>10,000 [a]	Partial, 50%	597	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/E95A/Q126D)	229	106 [a]	Inactive	>10,000 on graph, NC [a]	Inactive

NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

TABLE 19

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 6 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (D20A/E61R)	230	3950 [a]	Partial, 10%	278	Partial, 50%
1H3-hIgG1-L6-hIL-2 (D20A/F42N)	247	>10,000 [a]	Partial, 50%	662	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/F42Q)	248	>10,000 on graph, NC [a]	Partial, 30%	630	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/F42I)	251	1307 [a]	Partial, 20%	494	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/F42L)	252	68	Full	533	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/F42M)	253	53	Full	370	Partial, 50%
1H3-hIgG1-L6-hIL-2 (D20A/F42P)	254	9374 [a]	Partial, 80%	702	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/F42S)	255	1286	Partial, 70%	687	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/F42T)	256	1474 [a]	Partial, 10%	622	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/F42W)	257	414 [a]	Partial, 70%	400	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/F42Y)	258	322	Partial, 70%	545	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/F42V)	259	5796 [a]	Partial, 30%	579	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/Y45A)	260	61	Partial, 80%	554	Partial, 80%
1H3-hIgG1-L6-hIL-2 (D20A/Y45N)	261	31	Full	390	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/Y45D)	262	363	Partial, 60%	729	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/Y45Q)	263	730 [a]	Partial, 70%	348	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/Y45E)	264	1414 [a]	Partial, 60%	486	Partial, 70%
1H3-hIgG1-L6-hIL-2 (D20A/Y45G)	265	613 [a]	Partial, 80%	392	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/Y45H)	266	420 [a]	Partial, 70%	427	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/Y45I)	267	39	Partial, 70%	137	Partial, 30%
1H3-hIgG1-L6-hIL-2 (D20A/Y45L)	268	11	Full	426	Partial, 70%

TABLE 19-continued

Fold change from rhIL-2 and agonistic activity on 1H3-hIgG1-L6-hIL-2 fusion proteins from Group 6 in a cell-based proliferation assay

Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
1H3-hIgG1-L6-hIL-2 (D20A/Y45M)	269	107	Full	449	Partial, 60%
1H3-hIgG1-L6-hIL-2 (D20A/Y45F)	270	25	Partial, 90%	272	Partial, 50%
1H3-hIgG1-L6-hIL-2 (D20A/Y45P)	271	577 [a]	Full	710	Full
1H3-hIgG1-L6-hIL-2 (I92D/F42Q)	277	7227 [a]	Partial, 30%	872	Full
1H3-hIgG1-L6-hIL-2 (I92D/F42I)	280	4587 [a]	Partial, 10%	3644 [a]	Full
1H3-hIgG1-L6-hIL-2 (I92D/F42K)	282	>10,000 [a]	Partial, 20%	848 [a]	Full
1H3-hIgG1-L6-hIL-2 (I92D/F42T)	286	>10,000 [a]	Partial, 40%	1068 [a]	Full
1H3-hIgG1-L6-hIL-2 (I92D/F42W)	287	405 [a]	Full	3954 [a]	Full
1H3-hIgG1-L6-hIL-2 (I92D/F42Y)	288	58	Full	106	Full
1H3-hIgG1-L6-hIL-2 (I92D/F42V)	289	1075 [a]	Partial, 60%	343	Full
1H3-hIgG1-L6-hIL-2 (I92D/Y45A)	290	15	Full	285	Full
1H3-hIgG1-L6-hIL-2 (I92D/Y45Q)	293	53	Full	80	Full
1H3-hIgG1-L6-hIL-2 (I92D/Y45G)	295	41	Full	91	Full
1H3-hIgG1-L6-hIL-2 (I92D/Y45M)	299	7	Full	146	Full
1H3-hIgG1-L6-hIL-2 (I92D/Y45F)	300	33	Full	1650 [a]	Full
1H3-hIgG1-L6-hIL-2 (I92D/Y45S)	302	20	Full	306	Full
1H3-hIgG1-L6-hIL-2 (R38E/D20H)	306	13	Inactive	2945	Partial, 40%
1H3-hIgG1-L6-hIL-2 (R38E/D20S)	307	>10,000 on graph, NC [a]	Partial, 50%	626	Full
1H3-hIgG1-L6-hIL-2 (F42A/N88R)	308	8351 [a]	Partial, 70%	1456	Full
1H3-hIgG1-L6-hIL-2 (F42A/N88D)	309	1966 [a]	Full	86	Full
1H3-hIgG1-L6-hIL-2 (R38E/I92K)	334	>10,000 [a]	Partial, 70%	239	Full
1H3-hIgG1-L6-hIL-2 (R38E/I92P)	337	>10,000 on graph, NC [a]	Inactive	>10,000 on graph, NC [a]	Inactive
1H3-hIgG1-L6-hIL-2 (R38E/H16E)	343	658 [a]	Full	58	Full
1H3-hIgG1-L6-hIL-2 (R38K/D20A)	344	66	Full	369	Partial, 70%

NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

Example 6: Generation of Anti-hPD-1 Antibodies

Several approaches were used to generate a variety of different anti-hPD-1 antibodies with desired properties.

In one approach, anti-hPD-1 human monoclonal antibodies were generated using transgenic chickens (OmniChicken™) that express human antibody genes (human light chain (VLCL or VKCK) and human VH) and the chicken constant regions of the heavy chain (Ching et al., mAbs 2018). Transgenic chickens were immunized with 100 μg of Fc-tagged human PD-1 protein (huPD-1-Fc) (SEQ ID NO: 380) every 14 days for 14 weeks. In another approach, transgenic chickens were genetically immunized six times with DNA encoding human PD-1 (SEQ ID NO: 347) followed by a final boost with 100 μg huPD-1-Fc (SEQ ID NO: 380). The serum immune response of each animal was monitored by ELISA against biotinylated human PD-1 on streptavidin coated plates.

Splenocytes were isolated from each immunized animal, tested for positive antibody clones using the Gel Encapsulated Microenvironment (GEM) assay (as described in Mettler Izquierdo, S., Varela, S., Park, M., Collarini, E. J., Lu, D., Pramanick, S., Rucker, J., Lopalco, L., Etches, R., & Harriman, W. (2016). High-efficiency antibody discovery achieved with multiplexed microscopy. *Microscopy (Oxford, England)*, 65 (4), 341-352) and screened against human PD-1 labelled beads. Positive clones were sequenced and variable regions of the heavy and light chains were cloned, assembled into a single chain variable fragment, and fused to the hinge and Fc regions of immunoglobulins (ScFv-Fc). These unique scFv-Fc fusion proteins were transiently expressed in Expi293 cells and supernatants were tested for binding activity by ELISA on plates coated with huPD-1-Fc (SEQ ID NO: 380) or cynomolgous-PD-1-Fc (SEQ ID NO: 381). In total, 102 unique anti-human PD-1 variable heavy and variable light pairings were identified using this method. 2H7-hIgG4 (SEQ ID NOs: 382-391, 424, and 425) and A2-hIgG4 (SEQ ID NOs: 402-411, 428, and 429) were among the antibodies identified in this approach.

Other approaches led to the identification of an anti-hPD-1 antibody denoted as C51E6-hIgG4, which was germline optimized to become the antibody designated C51E6-5-hIgG4 (SEQ ID NOs: 392-401, 426, 427), and humanized and further sequence optimized to become the antibody designated Abzlmod-hIgG4 (SEQ ID NOs: 449, 450).

The anti-PD-1 variable region sequences were expressed as human IgG4 kappa antibodies and were evaluated for the ability to bind to PD-1 expressing cells using flow cytometry as described in General Methods Protocol A. Antibodies to be tested were first screened for binding to human PD-1 using a Jurkat cell line expressing recombinant human PD-1 (Jurkat+hPD-1 cell line). Antibodies were serially diluted from a top concentration of 280 nM and Allophycocyanin-conjugated anti-human IgG secondary antibody was then added to cells for detection. Of 92 hits, 79 test anti-PD-1 antibodies had an EC_{50} binding (by flow cytometry) of <30 nM. 2H7-hIgG4 (SEQ ID NOs: 382-391, 424, and 425), C51E6-5-hIgG4 (SEQ ID NOs: 392-401, 426, and 427), A2-hIgG4 (SEQ ID NOs: 402-411, 428, and 429), OMC.1.B6-hIgG4 (SEQ ID NOs: 438 and 439), OMC.1.D6-hIgG4 (SEQ ID NOs: 442 and 443), OMC.2.C6-hIgG4 (SEQ ID NOs: 440 and 441), 1H9-hIgG4 (SEQ ID NOs: 576 and 525), 1D5-hIgG4 (SEQ ID NOs: 577 and 527), and 2A3.H7-hIgG4 (SEQ ID NOs: 424 and 523) were among a group of antibodies identified as antibodies with medium to high affinity binding to hPD-1 using a Jurkat cell line expressing human PD-1 (SEQ ID NO: 346). The calculated EC_{50} of binding to Jurkat cells which recombinantly

expressed hPD-1 by flow cytometry in multiple experiments was 0.1-0.3 nM for 2H7-hIgG4, 1H9-hIgG4, 1D5-hIgG4, and 2A3.H7-hIgG4. The calculated EC_{50} of binding to Jurkat cells expressing hPD-1 by flow for C51E6-5-hIgG4 was 2-4 nM, and 3-16 nM for A2-hIgG4, OMC.1.B6-hIgG4, OMC.1.D6-hIgG4, and OMC.2.C6-hIgG4. Binding was specific to hPD-1 since 2H7-hIgG4, C51E6-5-hIgG4, A2-hIgG4, 1H9-hIgG4, 1D5-hIgG4, 2A3.H7-hIgG4, OMC.1.B6-hIgG4, OMC.1.D6-hIgG4, and OMC.2.C6-hIgG4 antibody titrations did not bind the parental Jurkat cell line which did not express hPD-1 (data not shown).

Example 7: Characterization of Anti-hPD-1 Antibody Binding in the Presence of Anti-hPD-1 #1-mIgG2b-N297A and Anti-hPD-1 #2-mIgG2b-N297A Antibodies

2H7-hIgG4, C51E6-5-hIgG4, and A2-hIgG4 were assessed for binding competition to hPD-1 in the presence of anti-hPD-1 #1-mIgG2b-N297A and anti-hPD-1 #2-mIgG2b-N297A as described in General Methods Protocol B.

As a control, OPDIVO® (nivolumab) was titrated in the presence of saturating concentrations of 10 UM anti-hPD-1 #1-mIgG2b-N297A (FIG. **4**A). The dose-titration curve in the presence of anti-hPD-1 #1-mIgG2b-N297A competitor was greatly reduced (100 to 1000-fold shift of the dose-titration curve to the right of the graph) when compared to the dose-titration curve of OPDIVO® without anti-hPD-1 #1-mIgG2b-N297A competitor. The addition of anti-hPD-1 #1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N297A at saturating concentrations (10 μM) prior to exposure with 2H7-hIgG4, C51E6-5-hIgG4, or A2-hIgG4 did not abrogate binding of 2H7-hIgG4, C51E6-5-hIgG4, or A2-hIgG4 to hPD-1 as illustrated by less than 10-fold shift in FIG. **4**B-**4**D, suggesting that 2H7-hIgG4, C51E6-5-hIgG4 and A2-hIgG4 did not compete for binding to PD-1 in the presence of anti-hPD-1 #1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N297A.

Example 8: Characterization of Non-Antagonist hPD-1 Antibodies

Anti-hPD-1 antibodies 2H7-hIgG4, C51E6-5-hIgG4 and A2-hIgG4 were tested for PD-1 antagonist activity using an in vitro cell-based human PD-1/PD-L1 blockade bioassay as described in General Methods Protocol C. All antibodies except A2-hIgG4 were tested at 200 nM final concentration. A2-hIgG4 was tested at 500 nM final concentration.

None of the anti-hPD-1 antibodies 2H7-hIgG4, C51E6-5-hIgG4, A2-hIgG4, OMC.1.B6-hIgG4, OMC.1.D6-hIgG4, OMC.2.C6-hIgG4, 1H9-hIgG4, 1D5-hIgG4, and 2A3.H7-hIgG4 demonstrated hPD-1 antagonist activity, as all displayed luminescence levels of an average of 3000 relative luminescence units (RLU) and exhibited an RLU similar to the negative control KLH-C3-hIgG4 (data not shown). In contrast, the anti-hPD-1 #1, which is a known hPD-1 antagonist that blocks hPD-L1 (SEQ ID NO: 584) engagement with hPD-1, exhibited luminescence of above 14,000 RLU (data not shown).

Example 9: Anti-hPD-1-Attenuated hIL-2 Fusion Proteins Bind Jurkat Cells Expressing Human PD-1

In order to construct various antibody and antibody-attenuated hIL-2 fusion protein expression vectors, the corresponding polynucleotide encoding sequences of antibody, cytokines, cytokine receptors and linkers were generated and cloned into expression vectors. The antibodies or antibody fusion proteins were transiently expressed in Human Embryonic Kidney (HEK) 293 cells, then purified by affinity chromatography using Protein A- or Protein G-Sepharose. The purified proteins were concentrated and buffer-exchanged to phosphate buffered saline or phosphate buffered saline containing 100 mM L-arginine and 10 mM L-histidine using ultracentrifugal filtration, after which protein concentration was determined.

In some approaches, 2H7-hIgG4, C51E6-5-hIgG4, and A2-hIgG4 carrying an S228P hinge stabilization mutation were directly fused (df) to hIL-2 or fused to hIL-2 at the C-terminus of the immunoglobulin heavy chain using the L6 linker. An illustration of these anti-PD-1-attenuated hIL-2 fusion proteins is summarized in FIG. **5**. Various constructs were generated with the substitutions in hIL-2 that attenuated hIL-2 activity as described in Example 2. Anti-hPD-1-attenuated hIL-2 fusion proteins listed in Table 20 were tested for binding to hPD-1 using the Jurkat cell line expressing hPD-1 as described in General Methods Protocol A. The variable region of 2H7-hIgG4 (SEQ ID NOs: 384 and 385) was further optimized, and the isotype was switched to a human IgGIwith the effector function null substitutions L235A/G237A (LAGA, as described in WO1998/006248) to become H7-632-hIgG1-LAGA (SEQ ID NOs: 414 and 415). The optimized H7-632-hIgG1-LAGA was also directly fused (df) to a variant of hIL-2 with attenuated hIL-2 activity (hIL-2 T3A/D20A/R38E/C125A; SEQ ID NO: 217) to become H7-767 (SEQ ID NOs: 412-413, 415-423, 532) and both H7-632-hIgG1-LAGA and H7-767 were tested for binding to hPD-1 (Table 20). EC_{50} values were calculated from the geometric mean fluorescent intensity (gMFI) across the titrated concentrations using GraphPad Prism 7 software.

The generation of anti-hPD-1-attenuated hIL-2 fusion proteins did not reduce binding to hPD-1, and the anti-hPD-1-attenuated hIL-2 fusion proteins were still able to bind to Jurkat cells expressing human PD-1. The calculated EC_{50} of tested anti-hPD-1-attenuated hIL-2 fusion proteins in comparison to respective anti-hPD-1 antibody without the attenuated hIL-2 moiety is summarized in Table 20.

TABLE 20

Anti-hPD-1-attenuated hIL-2 fusion protein binding (EC_{50}) to hPD-1 expressing Jurkat cell line by flow cytometry

Anti-hPD-1 Antibody	EC_{50} (nM)	Corresponding Anti-hPD-1-hIL-2 Fusion Protein	EC_{50} (nM)
Anti-hPD-1 #1	0.3586	Anti-hPD-1 #1-hIgG4-L6-hIL-2 (D20A/R38E)	0.5318
C51E6-5-hIgG4	2.048	C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E)	1.587
OMC.1.B6-hIgG4	7.422	OMC.1.B6-hIgG4-L6-hIL-2 (D20A/R38E)	5.635
OMC.2.C6-hIgG4	11.52	OMC.2.C6-hIgG4-L6-hIL-2 (D20A/R38E)	16.32
OMC.1.D6-hIgG4	15.96	OMC.1.D6-hIgG4-L6-hIL-2 (D20A/R38E)	8.87

TABLE 20-continued

Anti-hPD-1-attenuated hIL-2 fusion protein binding (EC_{50}) to hPD-1 expressing Jurkat cell line by flow cytometry

Anti-hPD-1 Antibody	EC_{50} (nM)	Corresponding Anti-hPD-1-hIL-2 Fusion Protein	EC_{50} (nM)
A2-hIgG4	5.968	A2-hIgG4-df-hIL-2 (D20A/R38E)	10.67
D12-hIgG4	9.674	D12-hIgG4-df-hIL-2 (D20A/R38E)	17.09
G12-hIgG4	5.36	G12-hIgG4-df-hIL-2 (D20A/R38E)	7.578
2H7-hIgG4	0.2769	2H7-hIgG4-df-hIL-2 (D20A/R38E)	0.1946
H7-632-hIgG1-LAGA	0.115	H7-767	0.218

The addition of the attenuated hIL-2 moiety on anti-hPD-1 antibodies did not abrogate binding to human PD-1 as demonstrated by a less than 2-fold increase in EC_{50} binding of anti-hPD-1-hIL-2 fusion proteins to Jurkat+ hPD-1 cells in comparison to the anti-hPD-1 antibody without the attenuated hIL-2 moiety.

Example 10: Anti-hPD-1-Attenuated hIL-2 Fusion Proteins Bind hPD-1 in the Presence of Anti-hPD-1 #1 and Anti-hPD-1 #2 Antibodies

Anti-hPD-1-attenuated hIL-2 fusion proteins were tested for binding to the hPD-1 receptor in the presence of anti-hPD-1 #1 and anti-hPD-1 #2 as described in General Methods Protocol B and Example 7. The converse experiment was also performed in which anti-hPD-1 #1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N297A was examined for binding to hPD-1 in the presence of saturating concentrations of test antibody-attenuated hIL-2 fusion proteins. In this format, Jurkat cells expressing hPD-1 were plated at 100,000 cells per well in FACS buffer, blocked with anti-human FcγR Blocking Reagent (Miltenyi) for 10 minutes at 4° C. and washed. Test antibody-attenuated hIL-2 fusion proteins 2H7-hIgG4-df-hIL-2 (D20A/R38E), C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E), A2-hIgG4-df-hIL-2 (D20A/R38E), H7-767, and isotype control anti-DNase 1H3-hIgG4-df-hIL-2 (D20A/R38E) were diluted to 280 nM final concentration in 100 μL FACS buffer and incubated with Jurkat cells expressing hPD-1 cells for 1 hour on ice. Cells were washed and re-suspended in FACS buffer containing six-fold serial titrations of anti-hPD-1 #1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N297A starting at a maximum concentration of 50 nM for 1 hour on ice. Cells were washed and re-suspended in 1:100 dilution of Phycoerythrin-conjugated anti-mouse IgG light chain kappa monoclonal antibody for 45 minutes on ice. Cells were again washed and re-suspended in FACS buffer with 1:1000 dilution of Sytox Green (Thermo Fisher). Flow cytometry analysis was performed using the BD FACS Canto II (BD Biosciences) and gMFI calculated using FlowJo software version 10. EC_{50} values were calculated from the gMFI of the Phycoerythrin signal across the titrated concentrations using GraphPad Prism 7 software.

The addition of the attenuated hIL-2 to anti-hPD-1 antibodies 2H7-hIgG4, C51E6-5-hIgG4, and A2-hIgG4 did not diminish the ability of the anti-hPD-1 proteins to bind to human PD-1 in the presence of anti-hPD-1 #1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N297A, similar to the results described in Example 7 (FIG. **16**B-**16**D). H7-767 was also tested in this competition assay and FIG. **13**B illustrates that H7-767 continues to bind to the hPD-1 receptor in the presence of anti-hPD-1-#1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N297A. In contrast, the binding of the positive control anti-hPD-1 #1 was substantially decreased in the presence of anti-hPD-1 #1-mIgG2b-N297A or anti-hPD-1 #2-mIgG2b-N297A (FIG. **16**A, **13**A).

FIG. **6**A and FIG. **6**B show that for the converse competition assay, anti-hPD-1 #1-mIgG2b-N297A (FIG. **6**A) and anti-hPD-1 #2-mIgG2b-N297A (FIG. **6**B) were still able to bind to hPD-1 on Jurkat cells in the presence of saturating (280 nM) anti-hPD-1-attenuated hIL-2 fusion proteins 2H7-hIgG4-df-hIL-2 (D20A/R38E), C51E6-5-hIgG4-df-hIL-2 (D20A/R38E) or A2-hIgG4-df-hIL-2 (D20A/R38E). These binding curves with saturating anti-hPD-1-attenuated hIL-2 fusion proteins prior to exposure with anti-hPD-1 fusion proteins overlapped with binding curves of anti-hPD-1 #1-mIgG2b-N297A (no competition) or anti-hPD-1 #2-mIgG2b-N297A (no competition). The binding curves also overlapped with a saturating negative control fusion protein, 1H3-hIgG4-df-hIL-2 (D20A/R38E) that did not bind to hPD-1.

Example 11: Anti-hPD-1-Attenuated hIL-2 Fusion Proteins Bind Recombinantly-Expressed Cynomolgus PD-1

Anti-hPD-1-attenuated hIL-2 fusion proteins were tested in flow cytometry for binding to cynomolgus PD-1 using a human Embryonic Kidney 293 cell line expressing the SV40 large T cell antigen (HEK-293T) that was transiently transfected to recombinantly express cynomolgus PD-1. For each transfection reaction, 2 million HEK-293T cells were transfected with 2 μg of pCMV6-hygro-HA-cyno-PD-1 (1-185) (SEQ ID NO: 448), a mammalian vector comprising the cynomolgus PD-1 extracellular domain tagged with a human influenza hemagglutinin and the sequence encoding for hygromycin resistance. Transfection was performed by electroporation. Transfected cells were blocked with human FcγR blocking reagent and stained with titrating amounts of anti-hPD-1-attenuated hIL-2 fusion proteins. Additionally, Phycoerythrin conjugated anti-hemagglutinin clone 15B12 was added to cells to stain for transfected cells and Allophycocyanin-conjugated anti-human IgG Fc secondary clone HP6017 (BioLegend Cat #409306) was added to cells to stain bound antibody. The cells were analyzed on the BD Canto II and FlowJo software version 10 was used to gate on live, transfected (hemagglutinin-positive) cells and to calculate gMFI of the Allophycocyanin signal. EC_{50} values were calculated from the gMFI across the titrated concentrations using GraphPad Prism 7 software.

Anti-hPD-1-attenuated hIL-2 fusion proteins bound to cynomolgus PD-1-expressing HEK-293T cells in a similar fashion to the binding profile seen on Jurkat T cells expressing human PD-1 (FIG. **17**). The EC_{50} for binding to cynomolgus PD-1 expressing HEK-293T cells was 5 nM for 2H7-hIgG4-df-hIL-2 (D20A/R38E), 6 nM for C51E6-5-hIgG4-df-hIL-2 (D20A/R38E), and 11 nM for A2-hIgG4-df-hIL-2 (D20A/R38E). Anti-hPD-1 #1 and anti-hPD-1 #2

which were formatted as comparator anti-hPD-1-attenuated hIL-2 fusion proteins also bound to cynomolgus PD-1 with EC_{50} values of 9 nM and 2 nM, respectively, suggesting that the addition of the attenuated hIL-2 moiety on the anti-hPD-1 antibodies did not abrogate binding to cynomolgus PD-1.

Example 12: Anti-hPD-1-Attenuated hIL-2 Fusion Proteins Bind Activated Primary Human and Cynomolgus PD-1

The binding of anti-hPD-1 antibodies and anti-hPD-1-attenuated hIL-2 fusion proteins on activated primary T cells expressing hPD-1 was examined by flow cytometry. To test if 2H7-hIgG4, C51E6-5-hIgG4, or A2-hIgG4 bound to native hPD-1, cryopreserved human peripheral blood mononuclear cells (PBMCs) were thawed and activated with 50 ng/ml phorbol 12-myristate 13-acetate (PMA) and 1 μg/mL ionomycin to up-regulate the hPD-1 receptor. Activated PBMCs were collected, blocked with 1:50 dilution of Human FcγR Blocking Reagent (Miltenyi) for 10 minutes at 4° C., and stained with titrated concentrations of anti-hPD-1 antibodies 2H7-hIgG4, C51E6-5-hIgG4, A2-hIgG4, anti-hPD-1 #1, and isotype control. Cells were then stained with 1:20 dilution of Allophycocyanin-conjugated anti-human IgG Fc to detect bound antibody. To delineate immune subsets, a cocktail of surface markers included anti-human CD3, anti-CD4, and anti-CD8 antibodies was used. In addition, a sample fraction was examined for cellular expression of hPD-1, hCD25, hCD122, and hCD132. Cells were analyzed on the BD Fortessa (BD Biosciences), FlowJo software version 10 was used to gate on T cell subsets then calculate gMFI of the allophycocyanin signal. EC_{50} values were calculated from the gMFI across the titrated concentrations using GraphPad Prism 7 software. To test the binding of anti-hPD-1-hIL-2 fusion proteins, cryopreserved CD3+ T cells were activated with PMA/ionomycin and flow cytometry binding was performed identically as described above.

Human PD-1 antibody-attenuated hIL-2 fusion proteins were also tested for binding to activated cynomolgus T cells using flow cytometry. Cynomolgus PBMCs were activated with a mixture of 0.081 μM PMA and 1.34 μM ionomycin. 24 hours later, cells were stained using the same procedure as binding to human PD-1 primary cells described above except cynomolgus cross-reactive markers were used. FlowJo software version 10 was used to gate on live, $CD3^+CD4^+$ or $CD3^+CD8^+$ T cells and then to calculate gMFI of the Allophycocyanin signal. EC_{50} values were calculated from the gMFI across the titrated concentrations of anti-hPD-1 antibodies or hPD-1 antibody-attenuated hIL-2 fusion proteins using GraphPad Prism 7 software.

In some variants tested, the attenuated hIL-2 also included the substitutions T3A and C125A, which remove a site for O-linked glycosylation and substitute away a free cysteine residue, respectively.

40-50% of $CD4^+$ T cells were $PD\text{-}1^+$ while 30-40% of $CD8^+$ T cells were $PD\text{-}1^+$ after PMA and ionomycin activation (data not shown). The calculated EC_{50} for binding to activated human $CD3^+CD4^+$ T cells by flow cytometry was 0.1-0.7 nM for 2H7-hIgG4, 12 nM for C51E6-5-hIgG4, 30 nM for A2-hIgG4, and 0.04 nM for 2H7-hIgG4-df-hIL-2 (T3A/D20A/R38E/C125A). The EC_{50} for binding to activated human $CD3^+CD8+$ T cells was 0.1-0.8 nM for 2H7-hIgG4, 16 nM for C51E6-5-hIgG4, 22 nM for A2-hIgG4, and 0.03 nM for 2H7-hIgG4-df-hIL-2 (T3A/D20A/R38E/C125A). The EC_{50} for binding to activated human $CD3^+CD4^+$ T cells was 0.19 nM and activated human $CD3^+CD8^+$ T cells was 0.12 nM for H7-767. The EC_{50} for binding to activated cynomolgus $CD3^+CD4+$ T cells was 0.09 nM for 2H7-hIgG4 and 0.04 nM for 2H7-hIgG4-df-hIL-2 (T3A/D20A/R38E/C125A). EC_{50} for binding to activated cynomolgus $CD3^+CD8+$ T cells was 0.08 nM for 2H7-hIgG4 and 0.03 nM for 2H7-hIgG4-df-hIL-2 (T3A/D20A/R38E/C125A). The EC_{50} for binding to activated cynomolgus $CD3^+CD4^+$ T cells was 0.26 nM and activated cynomolgus $CD3^+CD8^+$ T cells was 0.24 nM for H7-767. This data demonstrated that when the hPD-1 antibodies were converted to anti-hPD-1-attenuated hIL-2 fusion proteins, the calculated EC_{50} value for binding to activated hPD-1 remained similar to the calculated EC_{50} value of hPD-1 naked antibody binding to hPD-1. H7-767 and H7-632-hIgG1-LAGA anti-PD-1 naked antibody were tested for binding on primary non-activated human $CD4^+$ and $CD8^+$ T cells by flow cytometry. Frozen human $CD3^+$ T were thawed and flow cytometry performed as described above. Both H7-767 and H7-632-hIgG1-LAGA anti-PD-1 naked antibody did not bind non-activated human $CD4^+$ and $CD8^+$ T cells (data not shown).

Example 13: Quantification of Binding of Anti-hPD-1 Antibodies and Anti-hPD-1-Attenuated hIL-2 Fusion Proteins to Recombinant Human or Cynomolgus PD-1 by Surface Plasmon Resonance (SPR)

Surface plasmon resonance binding analysis was performed using a high-throughput SPR Carterra® LSA™ to determine binding affinities of anti-hPD-1 antibodies and anti-hPD-1-attenuated hIL-2 fusion proteins. Proteins were diluted to 2 or 10 μg/mL in 10 mM sodium acetate pH 4.5 containing 0.01% Tween-20 and coupled to a HC30M (Carterra Bio) chip using sulpho-N-hydroxysuccinimide/1-ethyl-3-(3-dimethylamino) propyl carbodiimide (sulpho-NHS/EDC) coupling chemistry and blocked with ethanolamine. A non-regenerative kinetic coupling process was used to determine binding kinetics to commercially sourced recombinant His-tagged human PD-1 and His-tagged cynomolgus PD-1 (Acro Biosystems).

Anti-hPD-1 antibodies and anti-hPD-1-attenuated hIL-2 fusion proteins were expressed with either a modified human IgG1 or a modified IgG4 isotype with a kappa light chain framework. Additional substitutions L235E, or L235A/G237A (LAGA, as described in Int'l Pub. No. WO1998/006248) (numbering based upon the EU numbering system) were introduced to the Fc region to abrogate effector functions of the immunoglobulin component.

The association constants (k_a), dissociation constants (k_d), and equilibrium constants (K_D) of various anti-hPD-1 antibodies and anti-hPD-1 antibody-attenuated hIL-2 fusion proteins binding to recombinant human or cynomolgus PD-1 proteins was determined from the titration curves and the Carterra Kinetics software. The maximal feasible SPR signal generated (R_{max}) and residual standard deviation (Res SD) was also calculated. The results from the kinetics screen are summarized in Table 21, and demonstrated that the addition of the attenuated hIL-2 moiety on anti-hPD-1 antibodies did not modulate PD-1 antibody binding to the human PD-1 or cynomolgus PD-1 antigens. In a separate experiment, H7-632-hIgG1-LAGA (SEQ ID NOs: 414 and 415) was measured by SPR and had a steady state equilibrium dissociation constant (K_D) of 1.23×10^{-9}M and H7-767 had a K_D)=1.93×10^{-9}M.

TABLE 21

Binding kinetics of anti-hPD-1 and anti-hPD-1-hIL-2 fusion proteins to recombinant human PD-1 and cynomolgus PD-1 by high-throughput SPR Carterra ® LSA ™

		Kinetics Summary									
		Human PD-1					Cyno PD-1				
	Name	k_a (M−1 s−1)	k_d (s−1)	K_D (M)	Rmax	Res SD	k_a (M−1 s−1)	k_d (s−1)	K_D (M)	Rmax	Res SD
Anti-hPD-1 Anti-bodies	2H7-hIgG4-LE	2.60E+05	8.20E−04	3.10E−09	146	8.5	1.40E+05	1.00E−03	7.10E−09	186	6.5
	2H7-hIgG4-LAGA	1.70E+05	9.10E−04	5.30E−09	258	13	9.10E+04	1.10E−03	1.20E−08	295	11
	Abz1mod-hIgG4	1.40E+05	6.00E−05	4.26E−10	123	8.1	1.70E+05	6.20E−04	3.70E−09	183	10
	A2-hIgG4	3.70E+04	1.30E−03	3.60E−08	341	7.8	6.80E+04	4.00E−02	5.89E−07	238	4.8
	OMC.1.B6-hIgG4	7.70E+04	4.00E−03	5.20E−08	241	6.8	8.80E+04	4.40E−03	5.10E−08	262	5.5
	OMC.2.C6-hIgG4	5.70E+04	6.60E−04	1.20E−08	229	8.7	5.50E+04	7.40E−04	1.30E−08	268	8.9
	OMC.1.D6-hIgG4	4.10E+04	1.70E−03	4.20E−08	263	5.1	5.80E+04	4.00E−02	6.94E−07	182	4
	OMC476pH7-hIgG4	6.00E+04	1.10E−03	1.80E−08	225	8.9	7.80E+04	1.70E−02	2.21E−07	254	2.8
	OMC476pB11-hIgG4	5.00E+04	1.50E−03	3.00E−08	221	7	8.00E+04	2.60E−02	3.21E−07	204	2.7
	OMC476pG10-hIgG4	9.30E+04	4.10E−03	4.40E−08	256	4.9	1.20E+05	6.00E−02	4.87E−07	188	4.9
	OMC476pH10-hIgG4	1.00E+05	6.50E−03	6.40E−08	63	1.8	1.20E+05	5.90E−02	4.80E−07	81	3.8
	OMC476pE4-hIgG4	7.90E+04	8.80E−04	1.10E−08	216	9.6	1.00E+05	3.50E−02	3.31E−07	204	6.3
	D12-hIgG4	5.70E+04	4.60E−04	8.10E−09	234	9.9	5.90E+04	1.60E−02	2.72E−07	297	2.4
	G12-hIgG4	5.30E+04	2.60E−03	5.00E−08	477	8.5	8.60E+04	6.50E−02	7.54E−07	327	7.8
	EH12.2H7-mIgG1*	1.10E+05	2.20E−03	1.90E−08	309	5.2	8.60E+04	7.30E−03	8.50E−08	307	4.2
	J105-mIgG1*	6.20E+04	5.30E−03	8.60E−08	186	2.8	5.00E+04	6.60E−02	1.30E−09	92	1.2
	MIH4-mIgG1*	1.30E+05	1.40E−03	1.00E−08	117	3.8	1.30E+05	1.20E−01	8.91E−07	61	1.8
	J110-hIgG1	1.00E+05	1.00E−03	1.00E−08	346	15	4.10E+04	5.00E−02	1.20E−09	228	8.2
	OPDIVO ® (nivolumab)	1.70E+05	1.70E−03	1.00E−08	55	2.6	1.50E+05	9.50E−04	6.40E−09	75	3.2
	KEYTRUDA ® (pembrolizumab)	2.90E+05	1.30E−03	4.50E−09	19	2.6	7.00E+05	4.00E−04	5.75E−07	53	3.7
Anti-hPD-1-attenuated hIL-2 Fusion Proteins	2H7-hIgG1-LAGA-hIL-2 (T3A/D20A/R38E/C125A)	1.50E+05	8.30E−04	5.40E−09	420	28	8.80E+04	9.70E−04	1.10E−08	502	21
	2H7-hIgG4-LE-hIL-2 (T3A/D20A/R38E/C125A)	1.90E+05	8.10E−04	4.30E−09	374	17	9.00E+04	1.00E−03	1.10E−08	449	15
	2H7-hIgG4-LAGA-hIL-2 (T3A/D20A/R38E/C125A)	1.70E+05	8.20E−04	4.80E−09	359	22	9.60E+04	9.80E−04	1.00E−08	429	17
	2H7-hIgG1-LAGA-hIL-2 (T3A/R38E/192K/C125A)	1.80E+05	7.80E−04	4.30E−09	417	25	9.10E+04	9.70E−04	1.10E−08	505	19
	hIgG4-LE-hIL-2 (T3A/R38E/192K/C125A)	1.90E+05	8.80E−04	4.70E−09	380	19	9.50E+04	1.10E−03	1.20E−08	429	17
	2H7-hIgG4-LAGA-hIL-2 (T3A/R38E/192K/C125A)	2.20E+05	8.20E−04	3.70E−09	355	17	1.00E+05	1.10E−03	1.10E−08	418	16
	2H7-hIgG1-LAGA-hIL-2 (T3A/R38E/D84K/C125A)	1.30E+05	8.10E−04	6.20E−09	458	29	7.60E+04	1.00E−03	1.30E−08	532	23
	2H7-hIgG4-LE-hIL-2 (T3A/R38E/D84K/C125A)	2.00E+05	9.40E−04	4.70E−09	232	13	1.30E+05	1.10E−03	8.20E−09	262	10
	2H7 hIgG4LAGA-df-hIL-2 (T3A/R38E/D84K/C125A)	1.70E+05	7.30E−04	4.40E−09	400	20	8.10E+04	1.00E−03	1.30E−08	482	20

*Commercially sourced, no sequence available

Example 14: Determining Whether Anti-hPD-1 Antibodies and Anti-hPD-1-Attenuated hIL-2 Fusion Proteins Compete with Anti-hPD-1 #1 and Anti-hPD-1 #2 for Binding to PD-1 by Surface Plasmon Resonance (SPR)

Anti-hPD-1 and anti-hPD-1-attenuated hIL-2 fusion proteins were assayed for competition with one another using a sandwich method. Antibodies and corresponding antibody-IL-2 cytokine-fusion proteins were immobilized to HC30M chips using amine coupling chemistry described in Example 13. Following kinetic analysis described in Example 13, 80 nM human PD-1 (Acro Biosystems, Cat #PD-1-H5221-100 μg) was injected into the whole array. Competing anti-hPD-1 and anti-hPD-1-attenuated hIL-2 fusion proteins (analyte) were diluted to 30 μg/mL and subsequently injected into the array and binding parameters were assessed using SPR. Assessment of all anti-hPD-1 and anti-hPD-1-hIL-2 fusion proteins was performed in duplicate. Some variants tested had a modified human IgG1 or IgG4 kappa light chain framework with additional L235E or L235A/G237A (LAGA) substitutions to abrogate effector function of the immunoglobulin.

The screening of pairs of anti-hPD-1 or anti-hPD-1-attenuated hIL-2 fusion proteins allowed the identification of two bins, shown in Table 22. Antibodies and fusion proteins from Group 1 were able to bind hPD-1 in the presence of all antibodies and fusion proteins from Group 2, but competed with all members of the same Group. Antibodies and fusion proteins from Group 2 were able to bind hPD-1 in the presence of all antibodies and fusion proteins from Group 1, but competed with all members of the same Group. None of the anti-hPD-1 listed in Group 1 in Table 22 competed with KEYTRUDA® and OPDIVO®.

TABLE 22

Groups 1 and 2 from anti-hPD-1 and anti-hPD-1-attenuated hIL-2 fusion protein binning screen by SPR

Group 1	Group 2
Abz1mod-hIgG4	KEYTRUDA ®
OMC.1.B6-hIgG4	OPDIVO ®
OMC.1.D6-hIgG4	Anti-hPD-1 clone
OMC.2.C6-hIgG4	EH12.2H7-mIgG1*
OMC476pE4-hIgG4	Anti-hPD-1 clone

TABLE 22-continued

Groups 1 and 2 from anti-hPD-1 and anti-hPD-1-attenuated hIL-2 fusion protein binning screen by SPR

Group 1	Group 2
OMC476pH7-hIgG4	J105-mIgG1*
OMC476pB11-hIgG4	
OMC476pH10-hIgG4	
OMC476pG10-hIgG4	
A2-hIgG4	
D12-hIgG4	
G12-hIgG4	
2H7-hIgG4-LE	
2H7-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	
2H7-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	
2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/I92K/C125A)	
2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A)	
2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A)	
2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/D84K/C125A)	
2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A)	
2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A)	
Anti-PD-1 clone MIH4 mIgG1	
Anti-PD-1 clone J110 hIgG1	

*Commercially sourced, no sequence available

Example 15: Antagonism of Anti-hPD-1-Attenuated hIL-2 Fusion Proteins to hPD-1 in the Presence of Anti-hPD-1 #1 and Anti-hPD-1 #2

Anti-hPD-1-attenuated hIL-2 fusion proteins were tested for antagonism of hPD-1. Characterization of anti-hPD-1-attenuated hIL-2 fusion proteins was performed according to General Methods Protocol C. FIG. **7** illustrates these results. When compared to the PD-1 antagonists KEYTRUDA® or OPDIVO®, 2H7-hIgG4-df-hIL-2 (D20A/R38E), C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E), and A2-hIgG4-df-hIL-2 (D20A/R38E) were non-antagonistic to human PD-1, as demonstrated by the low level of detectable luminescence. H7-632-hIgG1-LAGA and H7-767 were also tested for antagonist activity as described in General Protocol C. FIG. **15** illustrates that H7-632-hIgG1-LAGA and H7-767 do not block hPD-L1 (SEQ ID NO: 584) from interacting with the hPD-1 receptor.

For competition assays using the cell-based co-culture assay described in General protocol C, a few modifications were performed. Samples of the anti-hPD-1-attenuated hIL-2 fusion proteins were diluted to a fixed concentration of 400 nM and 20 μL was added to 20 μL of titrated anti-hPD-1 #1 or anti-hPD-1 #2. The 40 μL mixture was added to CHO cells. Forty (40) μL of Jurkat PD-1 effector cells were overlayed on the mixture of CHO cells and anti-hPD-1-attenuated hIL-2 fusion proteins. In this competition assay, a final concentration of saturating 100 nM anti-hPD-1-attenuated hIL-2 fusion proteins was tested in combination with titrated anti-hPD-1 #1 or anti-hPD-1 #2. The rest of the assay was performed as described in General Protocol C. FIG. **18**A and FIG. **18**B demonstrate that the addition of 100 nM anti-hPD-1-attenuated hIL-2 fusion proteins did not compete with the blocking of titrated anti-hPD-1 #1 binding to hPD-L1 (SEQ ID NO: 584). Dose-titration curves of anti-hPD-1 #1 remained unchanged from curves without competitor antibody, suggesting that the presence of anti-hPD-1-attenuated hIL-2 fusion proteins did not compete with anti-hPD-1 #1 function even at high concentrations. In the presence of 100 nM 2H7-hIgG4-df-hIL-2 (D20A/R38E) and 100 nM C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E), anti-hPD-1 #2 exhibited a 35% reduction in luminescence (RLU) at higher concentrations of anti-hPD-1 #2 (FIG. **18**B) but it is unclear if this reduction was significant due to the extent of the standard deviation.

In the converse experiment, either anti-hPD-1 #1 or anti-hPD-1 #2 were diluted to a concentration of 400 nM and 20 μL was combined with 20 μL of titrated anti-hPD-1-attenuated hIL-2 fusion proteins. Anti-hPD-1-attenuated hIL-2 fusion proteins were serially titrated and the 40 μL mixture was added to CHO cells, then overlayed with 40 μL of Jurkat PD-1 Effector cells. The rest of the assay was performed as described in General Protocol C. FIG. **18**C and FIG. **18**D demonstrate that the addition of 100 nM anti-hPD-1 #1 (FIG. **18**C) or 100 nM anti-hPD-1 #2 (FIG. **18**D) do not impair the ability of the anti-hPD-1-attenuated hIL-2 fusion proteins to be antagonists. The observed flat curve above 18,000 relative luminescent units (RLU) indicated that there was no competition for antagonist activity and the anti-hPD-1-attenuated hIL-2 fusion proteins tested remained able to exhibit antagonist function even in the presence of anti-hPD-1 #1 or anti-hPD-1 #2.

Example 16: Testing Anti-hPD-1-Attenuated hIL-2 Fusion Proteins for Attenuation on the High-Affinity and Intermediate-Affinity hIL-2 Receptors with Cell-Based Proliferation Assays

Anti-hPD-1-attenuated hIL-2 fusion proteins were evaluated for the level of attenuation of hIL-2 activity using the cell proliferation assays on NK-92 and TF1+IL-2Rβ cell lines as described in General Protocol E. Control fusion proteins included fusion proteins incorporating an anti-DNase I antibody (designated 1H3) with a human IgG4 or human IgG1 backbone directly fused to hIL-2 or with a linker (SEQ ID NO: 355) to demonstrate the effects of non-targeting attenuated hIL-2 fusion proteins. The hIL-2 sequence of these constructs contained substitutions for attenuated hIL-2 activity as described in Example 2. Full, partial, or no agonistic IL-2 activity (inactive) was also assessed similarly to Example 3. Some of the variants tested were expressed on a modified human IgG1 or IgG4 isotype with a kappa light chain, with additional L235E or L235A/G237A (LAGA) substitutions in the Fc region to abrogate immunoglobulin effector function. In some antibody-cytokine fusion proteins, the hIL-2 cytokine was fused to the C-terminus of the light chain (LC fusion).

The calculated EC_{50} of each antibody-cytokine fusion protein was determined from relative luminescence units (RLU), and fold change EC_{50} was calculated when compared with recombinant human IL-2 (rhIL-2). The fold change from rhIL-2 and agonistic activity is summarized in Table 23. Agonistic activity was measured as full, partial, or inactive as determined by the maximal luminescence of antibody-attenuated hIL-2 fusion proteins in comparison to the maximal luminescence of rhIL-2. Antibody-attenuated hIL-2 fusion proteins dose-titration curves that reached the maximal luminescence as the rhIL-2 were considered to be variants with full activity. Partial activity was calculated as a percentage of full activity using rhIL-2 maximal luminescence as 100%. Maximal RLU of antibody-attenuated hIL-2

fusion proteins with less than 10% of the rhIL-2 maximal RLU at the highest concentration of 1200 nM were considered to have no agonist activity or inactive. For some variants EC_{50} values were estimated only since maximal luminescence was not reached, as annotated by an [a] in Table 23.

TABLE 23

Fold change from rhIL-2 and agonistic activity of antibody-attenuated hIL-2 fusion proteins on NK-92 (high-affinity IL-2R) and TF1 + IL-2Rβ (intermediate-affinity IL-2R) cell lines.

	Variants	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
Non-Targeted Antibody-Attenuated hIL-2 Fusion Proteins	1H3-hIgG4-df-hIL-2 (WT)	0 [a]	Full	0-1	Full
	1H3-hIgG4-L6-hIL-2 (WT)	0 [a]	Full	0-1	Full
	1H3-hIgG4-df-hIL-2 (WT) LC fusion	0 [a]	Full	24	Full
	1H3-hIgG4-L6-hIL-2 (WT) LC fusion	0 [a]	Full	2	Full
	1H3-hIgG4-L6-hIL-2 (D20Y)	>10,000 on graph, NC [a]	Inactive	>10,000 on graph, NC [a]	Inactive
	1H3-hIgG4-df-hIL-2 (D20Y)	>10,000 on graph, NC [a]	Partial, 60%	>10,000 on graph, NC [a]	Inactive
	1H3-hIgG1-df-hIL-2 (D20Y)	8539 [a]	Partial, 90%	>10,000 on graph, NC [a]	Inactive
	1H3-hIgG4-L6-hIL-2 (D20A/R38P)	>10,000 [a]	Partial, 80%	4132 [a]	Full
	1H3-hIgG4-L6-hIL-2 (D20A/R38S)	>10,000 on graph, NC [a]	Partial, 90%	9225 [a]	Full
	1H3-hIgG4-L6-hIL-2 (D20A/R38D)	118 [a]	Partial, 90%	8591 [a]	Partial, 90%
	1H3-hIgG4-L6-hIL-2 (D20A/R38Q/E95A)	153	Full	5738 [a]	Full
	1H3-hIgG4-L6-hIL-2 (D20A/F42H/E95A)	>10,000 [a]	Full	1368 [a]	Full
	1H3-hIgG4-L6-hIL-2 (R38D/I92D)	190	Full	437	Full
	1H3-hIgG4-L6-hIL-2 (R38E/I92D)	377 [a]	Full	296	Full
	1H3-hIgG4-L6-hIL-2 (F42H/I92D)	794 [a]	Full	393	Full
	1H3-hIgG4-df-hIL-2 (D20A/R38E)	868 [a]	Partial, 90%-Full	>10,000 [a]	Partial, 70%-Full
	1H3-hIgG4-L6-hIL-2 (D20A/R38E)	177 [a]	Partial, 60-80%	>10,000 [a]	Partial, 70%-Full
	1H3-hIgG4-L6-hIL-2 (T3A/D20A/R38E)	>10,000 on graph, NC [a]	Partial, 40%	>10,000	Partial, 70%
	1H3-hIgG4-L6-hIL-2 (D20A/R38E/C125A)	>10,000 [a]	Partial, 20%	6436	Partial, 40%
	1H3-hIgG4-L6-hIL-2 (T3A/D20A/R38E/C125A)	>10,000 on graph, NC [a]	Partial, 20%	>10,000	Full
	1H3-hIgG1-L6-hIL-2 (D20A/R38E)	NT	NT	250-372	Full
	1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E)	392	Partial, 80%	186	Partial, 60%
	1H3-hIgG1-L6-hIL-2 (D20A/R38E/C125A)	2346 [a]	Partial, 80%	2157 [a]	Partial, 60%
	1H3-hIgG4-df-hIL-2 (D20A/R38E) LC fusion	>10,000 on graph, NC [a]	Inactive	>10,000 on graph, NC [a]	Inactive
	1H3-hIgG4-L6-hIL-2 (D20A/R38E) LC fusion	>10,000 on graph, NC [a]	Inactive	2155 [a]	Partial, 30%
	1H3-hIgG1-L6-hIL2 (H16A)	0	Full	0 [a]	Full
	1H3-hIgG1-L6-hIL2 (F42A)	0	Full	0 [a]	Full
	1H3-hIgG1-L6-hIL2 (H16A/F42A)	1	Full	0 [a]	Full
Anti-hPD-1-Attenuated hIL-2 Fusion Proteins	A2-hIgG4-df-hIL-2 (D20A/R38E)	811 [a]	Partial, 20-90%	>10,000 [a]	Partial, 60-80%
	D12-hIgG4-df-hIL-2 (D20A/R38E)	>10,000 on graph, NC [a]	Partial, 20%	>10,000 [a]	Partial, 40%
	G12-hIgG4-df-hIL-2 (D20A/R38E)	>10,000 [a]	Partial, 20%	>10,000 [a]	Partial, 50%
	OMC476pB11-hIgG4-df-hIL-2 (D20A/R38E)	>10,000 on graph, NC [a]	Partial, 70%	36	Full
	OMC476pE4-hIgG4-df-hIL-2 (D20A/R38E)	>10,000 on graph, NC [a]	Partial, 70%	1619	Full
	OMC476pG10-hIgG4-df-hIL-2 (D20A/R38E)	>10,000 [a]	Partial, 70%	NC [a]	Inactive
	OMC476pH10-hIgG4-df-hIL-2 (D20A/R38E)	>10,000 on graph, NC [a]	Partial, 70%	3563 [a]	Partial, 80%
	A2-hIgG4-df-hIL-2 (D20A/F42A)	284	Full	4323 [a]	Partial, 80%
	A2-hIgG4-df-hIL-2 (D20A/F42S)	3542	Full	4052 [a]	Partial, 90%
	A2-hIgG4-df-hIL-2 (D20S/R38E)	NT	NT	7035 [a]	Full
	A2-hIgG4-df-hIL-2 (F42A/N88R)	6423	Full	3757 [a]	Partial, 90%
	A2-hIgG4-df-hIL-2 (F42I/I92D)	9543	Full	5611 [a]	Partial, 90%
	A2-hIgG4-df-hIL-2 (F42Q/I92D)	8572	Full	3363 [a]	Full
	A2-hIgG4-df-hIL-2 (F42T/I92D)	2175	Full	5649 [a]	Full
	A2-hIgG4-df-hIL-2 (F42W/I92D)	1239	Full	4409 [a]	Partial, 50%
	A2-hIgG4-df-hIL-2 (R38E/D84K)	160-1503	Full	1158-1716	Partial, 90%
	A2-hIgG4-df-hIL-2 (R38E/I92K)	252-977	Full	864-1655	Partial, 80%-Full
	C51E6-5-hIgG4-df-hIL-2 (D20A/R38E)	4317	Partial, 70%	>10,000 [a]	Partial, 60%
	C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E)	NT	NT	>10,000 [a]	Partial, 80%

TABLE 23-continued

Fold change from rhIL-2 and agonistic activity of antibody-attenuated hIL-2 fusion proteins on NK-92 (high-affinity IL-2R) and TF1 + IL-2Rβ (intermediate-affinity IL-2R) cell lines.

Variants	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
C51E6-5-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	4326	Partial, 80%	>10,000 [a]	Partial, 70%
C51E6-5-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	4336	Partial, 60%	>10,000 on graph, NC [a]	Partial, 60%
OMC.1.B6-hIgG4-L6-hIL-2 (D20A/R38E)	NT	NT	8460 [a]	Partial, 70%
OMC.1.D6-hIgG4-L6-hIL-2 (D20A/R38E)	NT	NT	>10,000 [a]	Partial, 70%
OMC.2.C6-hIgG4-L6-hIL-2 (D20A/R38E)	NT	NT	>10,000 [a]	Partial, 70%
2A3.H7-hIgG4-df-hIL-2 (D20A/R38E)	NT	NT	6603 [a]	Partial, 60%
1H9-hIgG4-df-hIL-2 (D20A/R38E)	NT	NT	9769 [a]	Partial, 90%
1D5-hIgG4-df-hIL-2 (D20A/R38E)	NT	NT	7420 [a]	Partial, 80%
1D5-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	NT	NT	NC [a]	Inactive
1D5-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	NT	NT	NC [a]	Partial, 20%
2H7-hIgG1-df-hIL-2 (T3A/D20A/R38E/C125A)	4839 [a]	Full	2057 [a]	Full
2H7-hIgG1-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	7727 [a]	Full	6729 [a]	Partial, 80%
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	>10,000 [a]	Full	3428 [a]	Partial, 50-60%
2H7-hIgG4-df-hIL-2 (T3A/D20A/R38E/C125A)	707-7206 [a]	Full	>10,000 [a]	Partial, 60%-Full
2H7-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	>10,000	Full	>10,000 [a]	Partial, 50-60%
2H7-hIgG4-LAGA-df-hIL-2 T3A/D20A/R38E/C125A)	>10,000	Full	7480 [a]	Partial, 40-50%
H7-767	>10,000 [a]	Partial, Full	>10,000 [a]	Full
2H7-hIgG1-df-hIL-2 (T3A/R38E/D84K/C125A)	1500	Partial, 90%	140 [a]	Full
2H7-hIgG1-LE-df-hIL-2 (T3A/R38E/D84K/C125A)	1268	Partial, 90%	517 [a]	Full
2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A)	2157-4035	Partial, 90%-Full	774-1650 [a]	Full
2H7-hIgG4-df-hIL-2 (T3A/R38E/D84K/C125A)	1602	Partial, 90%	>10,000 [a]	Full
2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/D84K/C125A)	1675-5096	Partial, 90%	1281-2842 [a]	Full
2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A)	1596-5689	Partial, 90%-Full	1203-3515 [a]	Partial, 60-80%
2H7-hIgG1-df-hIL-2 (T3A/R38E/I92K/C125A)	370	Full	160	Full
2H7-hIgG1-LE-df-hIL-2 (T3A/R38E/I92K/C125A)	319	Full	656	Full
2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A)	406-1280	Full	514-1569 [a]	Full
2H7-hIgG4-df-hIL-2 (T3A/R38E/I92K/C125A)	520	Full	789-926	Partial, 80%-Full
2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/I92K/C125A)	610-1675	Full	474-2080 [a]	Full
2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A)	827-2888	Full	737-2845 [a]	Partial, 70%-Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/D20S/R38E/C125A)	6689	Full	9711 [a]	Partial, 70%
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/D84F/C125A)	6199	Full	3915	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192R/C125A)	75	Full	89	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192E/C125A)	118	Full	53	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192S/C125A)	9	Full	30	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/I92D/C125A)	2717	Full	3396 [a]	Partial, 80%
2H7-hIgG1-LAGA-df-hIL2 (T3A/H16E/R38E/C125A)	126	Full	122	Full

NT = Not Tested

NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

Example 17: Rescue of IL-2 Activity of Anti-hPD-1-Attenuated hIL-2 Fusion Proteins on a Cell Line Expressing the Intermediate-Affinity hIL-2 Receptor and hPD-1

Anti-hPD-1-attenuated hIL-2 fusion proteins were evaluated for rescue of hIL-2 activity using a targeted cell line expressing hPD-1. Briefly, the TF1+IL-2Rβ cell line described in General Methods Protocol D was modified through lentiviral transduction to express the hPD-1 receptor (SEQ ID NO: 580). Flow cytometry with a Brilliant Blue 515 conjugated hPD-1 antibody (BD Biosciences Cat #565936) was used to detect hPD-1 expressing TF1+IL-2Rβ cells. Cells were sorted for low hPD-1 expression (less than 10^3 intensity on the Brilliant Blue 515 fluorophore). The pool was sorted twice more to collect cells that approximated hPD-1 expression levels on activated primary cells. This cell line (TF1+IL-2Rβ+hPD-1) was expanded and frozen in aliquots for the cell-based proliferation assays. Proliferation assays were performed as described in General Methods Protocol E with an incubation period of 3 days. Some variants tested had a modified human IgG1 or IgG4 kappa light chain framework with additional L235E or L235A/G237A (LAGA) substitutions to abrogate effector function of the immunoglobulin.

Table 24 summarizes the results from the proliferation assays on the targeted TF1+IL-2Rβ+hPD-1 cell line. Agonistic activity was measured as full, partial, or inactive as determined by the maximal luminescence of antibody-attenuated hIL-2 fusion proteins in comparison to the maximal luminescence of rhIL-2. Antibody-attenuated hIL-2 fusion protein dose-titration curves that reached the maximal luminescence as the rhIL-2 were considered to be variants with full activity. Partial activity was calculated as a percentage of full activity using rhIL-2 maximal luminescence as 100%. Maximal RLU of antibody-attenuated hIL-2 fusion proteins with less than 10% of the rhIL-2 maximal RLU at the highest concentration of 1200 nM were considered to have no agonist activity or inactive. For some variants, EC_{50} values were estimates only since a full curve was not reached. Many examples of anti-hPD-1-hIL-2 fusion proteins with attenuated hIL-2 showed rescued hIL-2 activity on the targeted cell line where the non-targeting antibody controls (denoted with 1H3) demonstrated no rescue of hIL-2 activity. Full rescue was illustrated by the reduction of fold-change from rhIL-2 to a value of 0 or 1.

TABLE 24

Fold change from rhIL-2 and agonistic activity of antibody-hIL-2 fusion proteins on TF1 + IL-2Rβ + hPD-1 cell line (human PD-1 expressing cell line with intermediate-affinity IL-2R).

	Variants	Fold decrease from rhIL-2 (TF1 + IL-2Rβ + hPD-1)	Agonistic Activity (TF1 + IL-2Rβ + hPD-1)
Non-Targeted Antibody-Attenuated hIL-2 Fusion Proteins	1H3-hIgG4-df-hIL-2 (WT)	1	Full
	1H3-hIgG4-L6-hIL-2 (WT)	1	Full
	1H3-hIgG4-L6-hIL-2 (D20Y)	NC [a]	Inactive
	1H3-hIgG4-df-hIL-2 (D20Y)	NC [a]	Inactive
	1H3-hIgG4-L6-hIL-2 (D20A/R38P)	3074 [a]	Partial, 80%
	1H3-hIgG4-L6-hIL-2 (D20A/R38S)	4482 [a]	Partial, 80%
	1H3-hIgG4-L6-hIL-2 (D20A/R38D)	2964 [a]	Partial, 60%
	1H3-hIgG4-L6-hIL-2 (D20A/R38Q/E95A)	3538 [a]	Partial, 80%
	1H3-hIgG4-L6-hIL-2 (D20A/F42H/E95A)	657 [a]	Partial, 70%
	1H3-hIgG4-L6-hIL-2 (R38D/I92D)	1428 [a]	Full
	1H3-hIgG4-L6-hIL-2 (R38E/I92D)	1887 [a]	Full
	1H3-hIgG4-L6-hIL-2 (F42H/I92D)	2024 [a]	Full
	1H3-hIgG4-df-hIL-2 (D20A/R38E)	307-3628 [a]	Partial, 70%-Full
	1H3-hIgG4-L6-hIL-2 (D20A/R38E)	4883-5226	Partial, 70%-Full
	1H3-hIgG4-L6-hIL-2 (T3A/D20A/R38E)	9167 [a]	Partial, 80%
	1H3-hIgG4-L6-hIL-2 (D20A/R38E/C125A)	4714	Partial, 60%
	1H3-hIgG4-L6-hIL-2 (T3A/D20A/R38E/C125A)	4626	Partial, 60%
	1H3-hIgG1-L6-hIL-2 (D20A/R38E)	297	Full
	1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E)	513	Partial, 80%
	1H3-hIgG1-L6-hIL-2 (D20A/R38E/C125A)	3342	Partial, 80%
	1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E/C125A)	1081	Partial, 90%
	1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	6459	Full
	1H3-hIgG1-L6-hIL-2 (H16A)	4 [a]	Full
	1H3-hIgG1-L6-hIL-2 (F42A)	0 [a]	Full
	1H3-hIgG1-L6-hIL-2 (H16A/F42A)	2 [a]	Full
	1H3-hIgG1-L6-hIL-2 (D20T)	75 [a]	Full
	1H3-hIgG1-L6-hIL-2 (T3A/F42A/Y45A/L72G/C125A)	2 [a]	Full

TABLE 24-continued

Fold change from rhIL-2 and agonistic activity of antibody-hIL-2 fusion proteins on TF1 + IL-2Rβ + hPD-1 cell line (human PD-1 expressing cell line with intermediate-affinity IL-2R).

	Variants	Fold decrease from rhIL-2 (TF1 + IL-2Rβ + hPD-1)	Agonistic Activity (TF1 + IL-2Rβ + hPD-1)
Anti-hPD-1-Attenuated hIL-2 Fusion Proteins	A2-hIgG4-df-hIL-2 (D20A/R38E)	0-1 [a]	Full
	D12-hIgG4-df-hIL-2 (D20A/R38E)	1 [a]	Full
	G12-hIgG4-df-hIL-2 (D20A/R38E)	1 [a]	Full
	OMC476pB11-hIgG4-df-hIL-2 (D20A/R38E)	0 [a]	Full
	OMC476pE4-hIgG4-df-hIL-2 (D20A/R38E)	2 [a]	Full
	OMC476pG10-hIgG4-df-hIL-2 (D20A/R38E)	0 [a]	Full
	OMC476pH10-hIgG4-df-hIL-2 (D20A/R38E)	1 [a]	Full
	A2-hIgG4-df-hIL-2 (D20A/F42A)	2 [a]	Full
	A2-hIgG4-df-hIL-2 (D20A/F42S)	1 [a]	Full
	A2-hIgG4-df-hIL-2 (D20S/R38E)	0 [a]	Full
	A2-hIgG4-df-hIL-2 (F42A/N88R)	0 [a]	Full
	A2-hIgG4-df-hIL-2 (F42I/I92D)	9 [a]	Full
	A2-hIgG4-df-hIL-2 (F42Q/I92D)	5 [a]	Full
	A2-hIgG4-df-hIL-2 (F42T/I92D)	1 [a]	Full
	A2-hIgG4-df-hIL-2 (F42W/I92D)	4 [a]	Full
	A2-hIgG4-df-hIL-2 (R38E/D84K)	0-1 [a]	Full
	A2-hIgG4-df-hIL-2 (R38E/I92K)	0-1 [a]	Full
	C51E6-5-hIgG4-df-hIL-2 (D20A/R38E)	0-1 [a]	Partial, 70%-Full
	C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E)	1 [a]	Partial, 90%
	C51E6-5-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	1 [a]	Full
	C51E6-5-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	0 [a]	Full
	OMC.1.B6-hIgG4-L6-hIL-2 (D20A/R38E)	0 [a]	Partial, 60%
	OMC.1.D6-hIgG4-L6-hIL-2 (D20A/R38E)	0 [a]	Partial, 90%
	OMC.2.C6-hIgG4-L6-hIL-2 (D20A/R38E)	0 [a]	Partial, 60%
	2A3.H7-hIgG4-df-hIL-2 (D20A/R38E)	0 [a]	Full
	1H9-hIgG4-df-hIL-2 (D20A/R38E)	0 [a]	Full
	1D5-hIgG4-df-hIL-2 (D20A/R38E)	1 [a]	Full
	2H7-hIgG1-df-hIL-2 (T3A/D20A/R38E/C125A)	1 [a]	Full
	2H7-hIgG1-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	0	Full
	2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	1 [a]	Full
	2H7-hIgG4-df-hIL-2 (T3A/D20A/R38E/C125A)	1 [a]	Full
	2H7-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	1-4 [a]	Full
	2H7-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	1 [a]	Full
	H7-767	0-1 [a]	Full
	2H7-hIgG1-df-hIL-2 (T3A/R38E/D84K/C125A)	2 [a]	Full
	2H7-hIgG1-LE-df-hIL-2 (T3A/R38E/D84K/C125A)	1 [a]	Full
	2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A)	1 [a]	Full
	2H7-hIgG4-df-hIL-2 (T3A/R38E/D84K/C125A)	1 [a]	Full
	2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/D84K/C125A)	0-2 [a]	Full
	2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A)	1-3 [a]	Full
	2H7-hIgG1-df-hIL-2 (T3A/R38E/I92K/C125A)	1 [a]	Full
	2H7-hIgG1-LE-df-hIL-2 (T3A/R38E/I92K/C125A)	1 [a]	Full
	2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A)	1-2 [a]	Full

TABLE 24-continued

Fold change from rhIL-2 and agonistic activity of antibody-hIL-2 fusion proteins on TF1 + IL-2Rβ + hPD-1 cell line (human PD-1 expressing cell line with intermediate-affinity IL-2R).

Variants	Fold decrease from rhIL-2 (TF1 + IL-2Rβ + hPD-1)	Agonistic Activity (TF1 + IL-2Rβ + hPD-1)
2H7-hIgG4-df-hIL-2 (T3A/R38E/I92K/C125A)	1 [a]	Full
2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/I92K/C125A)	1 [a]	Full
2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A)	1 [a]	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/D20S/R38E/C125A)	Not Attenuated on graph; NC [a]	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/D84F/C125A)	0 [a]	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192R/C125A)	0 [a]	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192E/C125A)	2 [a]	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192S/C125A)	Not Attenuated on graph; NC [a]	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/C125A)	0 [a]	Full
2H7-hIgG1-LAGA-df-hIL2 (T3A/H16E/R38E/C125A)	>10,000 [a]	Full

NC = Not Calculated by GraphPad Prism 7

[a] = Fold change is an estimate only since a full four parameter logistic curve was not reached

Example 18: Evaluation of Surrogate Anti-hPD-1-Attenuated hIL-2 Fusion Proteins that Block or do not Block Mouse PD-L1 in an In Vivo Murine Colon Adenocarcinoma (MC38) Model

Since there are no accepted models to explore in vivo efficacy of oncology therapeutics in primates, a surrogate anti-mPD-1-attenuated hIL-2 fusion protein was generated and tested in a syngeneic murine tumor model. This MC38 colon adenocarcinoma model is routinely used to test efficacy of immuno-oncology therapeutics. To explore the in vivo effect of the anti-PD-1-attenuated hIL-2 fusion protein, a surrogate anti-mouse PD-1 antibody designated RMP1-14 (known to block mouse PD-L1 binding) and RMP1-30 (described as a mouse PD-L1 non-blocker) was fused to an attenuated hIL-2 at the C-terminus of the mouse IgG2b-N297A heavy chain and tested in an MC38 colon adenocarcinoma model. The hIL-2 moiety included the substitutions F42K, Y45R, and V69R that were tested on an IL-2 dependent mouse T lymphoblast cell line (CTLL-2) and that were demonstrated to be attenuated for mouse IL-2 activity. Human IL-2 can stimulate proliferation of mouse T cells at similar concentrations, however the same substitutions that attenuate activity on human IL-2 dependent cell lines do not attenuate activity on the CTLL-2 cell line (data not shown). As such, the F42K/Y45R/V69R substitutions were used in hIL-2 as a surrogate since they demonstrated attenuated IL-2 activity on mouse cell lines. Sequences comprising the heavy and light chain variable region sequences of anti-mouse PD-1 antibodies RMP1-14 and RMP1-30 (as described in Matsumoto K et al., J Immunol. 2004 Feb. 15; 172 (4): 2530-41) were also formatted onto a murine IgG2b-N297A background to generate anti-mPD-1 RMP1-14 mIgG2b-N297A (SEQ ID NOs: 564 and 566) and anti-mPD-1 RMP1-30 mIgG2b-N297A (SEQ ID NOs: 567 and 568). The mouse IgG2b isotype with an N297A substitution is the murine equivalent of an Fc isotype that abrogates Fc immune effector function. Surrogate antibodies and anti-body-attenuated hIL-2 fusion proteins were produced, expressed and Protein-A purified using standard techniques.

In this murine tumor model, ten week old female C57BL/6NCrl (Charles River) mice were injected into the right flank with 5×10^5 MC38 colorectal carcinoma cells. When tumors reached 80-120 mm^3. mice were sorted into cohorts (10 mice/group) and treatment began on day 1 of study. Anti-mPD-1 RMP1-14 mIgG2b-N297A. anti-mPD-1 RMP1-30 mIgG2b-N297A. anti-mPD-1 RMP1-14 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) (SEQ ID NOs: 565 and 566), and anti-mPD-1 RMP1-30 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) (SEQ ID NOs: 568 and 569) were dosed intraperitoneally at 5 mg/kg twice weekly for 4 weeks along with vehicle control (phosphate-buffered saline). Tumor size was measured with calipers twice weekly using the formula $(w^2\times L)/2$ where w=width and L=length for the duration of the study. The study endpoint was a tumor volume of 1000 mm^3 or survival at day 50, whichever came first.

FIG. **8** demonstrates that although the administration of anti-mPD-1 RMP1-14-mIgG2b-N297A or anti-mPD-1 RMP1-30-mIgG2b-N297A antibodies alone did not promote significant efficacy relative to treatment with vehicle control, the administration of anti-mPD-1 RMP1-14 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) or anti-mPD-1 RMP1-30 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) anti-PD-1-attenuated hIL-2 fusion proteins was associated with 90% and 100% complete tumor regressions respectively. These data demonstrate that the anti-tumor efficacy mediated by anti-mPD-1-hIL-2 (F42K/Y45R/V69R) fusion proteins does not require PD-1 checkpoint blockade and that efficacy is dependent on hIL-2 activity. The data further demonstrate that antibody mediated targeting of PD-1 expressing T cells is sufficient to promote potent anti-tumor efficacy in the MC38 tumor model.

Example 19: Surrogate Anti-hPD-1-Attenuated hIL-2 Fusion Protein Expands Effector Memory CD8+ T Cells in an In Vivo Murine Colon Adenocarcinoma Model

To understand the mechanism-of-action of the surrogate anti-hPD-1-attenuated hIL-2 fusion protein in vivo, a similar in vivo experiment to Example 18 was performed, followed by immunophenotyping of the resultant T cell populations in tumors, blood, spleens and lymph nodes after three doses. Ten week old female C57BL/6NCrl (Charles River) mice were subcutaneously implanted with the 5×10^5 murine MC38 colon adenocarcinoma cancer tumor cells into the right flank and tumors were monitored for growth. Animals with tumors between 150-260 mm^3 were divided between four groups with 10 mice per group for the study. After 21 days post-implantation, animals were dosed intraperitoneally with 0.2 mL/dose phosphate buffered saline (PBS) for the vehicle control, 5 mg/kg anti-KLH-C3-mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R), 5 mg/kg anti-mPD-1 RMP1-30 mIgG2b-N297A, or 5 mg/kg anti-mPD-1 RMP1-30 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) on days 1, 4 and 8. On day 9, tumors, spleens and inguinal lymph nodes were harvested from all mice and processed into single cell suspensions for subsequent flow cytometry analysis.

FIG. **9**A charts the tumor volume growth (mm^3) over 9 days from the first dose on day 1 where each point represents a mean of 10 mice. By day 8, anti-mPD-1 RMP1-30 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) had a reduction in tumor volume compared to other treatment groups. FIG. **9**B summarizes the contribution of various $CD8^+$ T cell subsets in the tumor of each treatment group in which T Central Memory were phenotyped as $CD45^+CD3^+CD4^-CD8^+CD44^+CD127^+CD69^-CD103^-$. T Effector Memory were $CD45^+CD3^+CD4^-CD8^+CD44^+CD127^+CD69^+CD103^-CD62L^-$. T Resident Memory were $CD45^+CD3^+CD4^+CD8^+CD44^+CD127^+CD69^+CD103^+$, $CD44^+CD62L^-$ T cells were $CD45^+CD3^+CD4^-CD8^+CD44^+CD62L^-$ and T Naïve were $CD45^+CD3^+CD4^+CD8^+CD44^-CD62L^+$. In comparison to other treatment groups, there was expansion of the $CD8^+$ T Effector Memory subset in the anti-mPD-1 RMP1-30 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) treated mice as indicated in the increase of the light grey slice of FIG. **9**B. This was also illustrated in FIG. **9**C in absolute counts (cells/μL) within the MC38 dissected tumor. Furthermore, within the tumor, there was a decrease in the absolute counts (cells/μL) of Regulatory T cells defined as expressing $CD45^+CD3^+CD4^+CD8^+CD25^+FoxP3^+$ markers.

The expansion of $CD8^+$ T Effector Memory and decrease in Regulatory T cells has been associated with effective immunotherapy in both mice and humans.

Example 20: Anti-hPD-1-Attenuated hIL-2 Fusion Proteins are Active In Vivo in an NCG-PBMC Model

Engrafting human immune cells into NOD-$Prkdc^{em2Cd52}$IL-$2rg^{em26Cd22}$/NjuCrl (NCG) mice that lack functional T. B, and NK cells has been a valuable tool for evaluating efficacy of therapeutics hypothesized to stimulate human T cells. In this model, if the therapeutic activates human T cells, there would be a resulting expansion of T cells and accelerated graft-versus-host disease (GvHD).

Three independent donors for human peripheral mononuclear cell (hPBMC) engraftment were evaluated over a 4 week period for engraftment kinetics as well as expression of human PD-1 and human IL-2 receptors on T cells. Of the three donors tested. the donor that induced the most T cells with an intermediate window for GvHD was chosen. 1.5×10^7 hPBMCs were intravenously injected into NCG mice and divided into 8 groups of 8-16 mice. On days 7, 10, and 14, mice were intraperitoneally injected with three doses of 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) (SEQ ID NOs: 471, 425) (2.5 mg/kg, 5 mg/kg, or 10 mg/kg), 1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) (SEQ ID NOs: 546, 374) (5 mg/kg or 10 mg/kg), 1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A) (SEQ ID NOs: 563, 374) (10 mg/kg), or 2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/192K/C125A) (SEQ ID NOs: 474, 425) (5 mg/kg). The anti-DNase fusion protein both as a wild-type hIL-2 (1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A)) and with the attenuated hIL-2 moiety (1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)) was used as a non-targeting antibody control. Although the 1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A) fusion protein had no changes in the hIL-2 moiety which reduce hIL-2 activity, it did comprise the T3A and C125A substitutions to remove the predicted O-linked glycosylation site on human IL-2 (see for example Int'l Pub. No. WO2012/107417) and unpaired cysteine residue (see for example Int'l Pub. No. WO2018/184964), respectively. These substitutions have not demonstrated reduced hIL-2 potency in the clinic. On Day 21, blood, spleen, and lungs were harvested in which blood and spleens were processed for flow cytometry immunophenotyping while lungs were weighed.

After 21 days, flow cytometry immunophenotyping was performed on the blood and spleens of animals. Table 25 summarizes the markers used to delineate human T cell populations for subsequent analysis.

TABLE 25

Phenotypic markers to define human T cell subsets in NCG-PBMC mice

Cell Population	Phenotypic Markers
Pan T cells	CD3+
CD8+ Naïve	CD3+CD4−CD8+CD45RO−CCR7+
CD8+ Effector	CD3+CD4−CD8+CD45RO−CCR7−
CD8+ Effector Memory	CD3+CD4−CD8+CD45RO+CCR7−
CD8+ Central Memory	CD3+CD4−CD8+CD45RO+CCR7+
CD4+ Naïve	CD3+CD4+CD8−CD45RO−CCR7+
CD4+ Effector	CD3+CD4+CD8−CD45RO−CCR7−
CD4+ Effector Memory	CD3+CD4+CD8−CD45RO+CCR7−
CD4+ Central Memory	CD3+CD4+CD8−CD45RO+CCR7+
Regulatory T cells	CD3+CD4+CD8−CD25+Foxp3+
NK Cells	CD3−CD56+

Body weight was measured for 21 days and normalized to day 1 for each individual animal as an assessment of graft-versus-host disease (GvHD) as illustrated in FIG. **10**. Accelerated GvHD was observed in the 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) treated mice at 10 mg/kg. A small decrease in body weight was also observed in the 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) treated mice at 2.5 mg/kg, 5 mg/kg, and 2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/192K/C125A) at 5 mg/kg. Although body weight loss was seen in the 1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A), it was not sustained.

The flow cytometry analysis correlated with the accelerated graft-versus-host disease (GvHD) observed. Using the phenotypic markers for human T cell subset delineation provided in Table 25, flow cytometry analysis of peripheral blood demonstrated only a minor expansion of $CD3^+$, $CD4^+$, and $CD8^+$ T cell subsets (as quantified by a fold change from

vehicle control of between 10-fold to 50-fold for CD3+ T cells) in mice treated with 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) at 2.5 mg/kg and 5 mg/kg, and mice treated with 1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A) at 10 mg/kg. Furthermore, $CD3^+$, $CD4^+$, and $CD8^+$ T cell subsets were greatly expanded (fold change from vehicle control was greater than 50-fold for $CD3^+$ T cells) in the peripheral blood of mice treated with 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) at 10 mg/kg. Table 26 summarizes the expanded human T cell subsets.

TABLE 26

Expansion of human $CD3^+$, $CD4^+$, and $CD8^+$ T cell subsets in NCG-PBMC mice

	Fold Change in numbers (Blood)		
Agent	$CD3^+$ T cells	$CD4^+$ T cells	$CD8^+$ T cells
Vehicle (PBS)	1	1	1
1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A) 10 mg/kg	22.76	27.73	16.13
1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 5 mg/kg	1.94	2.12	1.74
1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 10 mg/kg	0.56	0.56	0.57
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 2.5 mg/kg	24.57	32.4	14.4
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 5 mg/kg	53.03	70.74	22.86
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) 10 mg/kg	203.3	296.94	58.82
2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A) 5 mg/kg	31.79	48.76	8.79

N/A = Not Applicable

In addition to evaluating $CD3^+$, $CD4^+$, and $CD8^+$ T cells between treatment groups, the memory and naïve subsets for $CD4^+$ and $CD8^+$ T cell subsets were also assessed. The phenotypic markers used for delineation of Naïve, Effector, Effector Memory and Central Memory for both $CD4^+$ and $CD8^+$ T cell is summarized in Table 25. There were no changes in Naïve, Effector or Central Memory T cells between treatment groups (data not shown). However, mice treated with 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) at 10 mg/kg had greatly expanded $CD4^+$ and $CD8^+$ Effector Memory (EM) T cells in the peripheral blood with an average cell number per milliliter greater than 5 million for $CD8^+$ T cells and greater than 50 million for $CD4^+$ T cells (FIGS. **11**A and **11**B). Box-and-whisker plots were graphed with the box around the first and third quartile, the horizontal line as the median, and lines indicated the minimum and maximum points. There was moderate expansion of $CD8^+$ Effector Memory (EM) T cells defined as an average cell number per million between 1 to 5 million per milliliter for animals treated with 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) at 2.5 mg/kg and 5 mg/kg as well as for 1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A). There was moderate expansion of $CD4^+$ Effector Memory (EM) T cells between 6 to 13 million per milliliter for $CD4^+$ T cells in the mice treated with 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) at 2.5 mg/kg and 5 mg/kg.

In addition to stimulating effector T cells, IL-2 has been described to stimulate NK cells and regulatory T cells (Tregs) and since Tregs express high levels of CD25 and NK cells express CD122, these immune cell types were also evaluated. FIG. **12** illustrates that animals treated with 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) at the highest dose of 10 mg/kg did not expand human regulatory T cells and instead had the lowest percent of regulatory T cells (as phenotypically defined in Table 25) in the peripheral blood of animals. There was a dose-dependent decrease of human regulatory T cells and in comparison to vehicle control that had an average of 1.6% human $CD3^+$ T cells that were Tregs, 2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) at 10 mg/kg had an average of 0.16% human $CD3^+$ T cells that were Tregs. There were no changes in the percentage of human NK cells in peripheral blood (phenotype defined in Table 25) in all treatment groups in comparison to vehicle control (data not shown).

Example 21: Non-Clinical Safety Profile of Anti-hPD-1-Attenuated hIL-2 Fusion Proteins

Cynomolgus monkeys previously have been used to evaluate the toxicity of unmodified IL-2. Lethality was observed in cynomolgus monkeys at exogenous recombinant IL-2 doses as low as 50 μg/kg/day. Since the binding of H7-767 to cynomolgus monkey hPD-1 on primary activated PBMCs was confirmed by flow cytometry (Example 12), a single-dose study for preliminary safety assessment was performed with both a variant of H7-767 (H7-02-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) (SEQ ID NOs: 582 and 583) and H7-767. H7-02-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) was delivered by 15 minute iv infusion to 8 monkeys at 1 mg/kg (4 animals) or 10 mg/kg (4 animals). Sampling at time-points up to 360 hours following infusion was performed. No adverse effects, gross toxicities, body weight loss, or lethality was observed (data not shown). A follow-up single-dose study using H7-767 was performed at higher doses of 5 mg/kg and 50 mg/kg similar to the first study, with sampling at time-points up to 360 hours post-infusion. Again, no adverse effects, gross toxicities, body weight loss or lethality was observed (data not shown).

Example 22: Attenuation of IL-2 Activity of Modified hIL-2 Proteins

The attenuation of IL-2 activity of modified hIL-2 proteins comprising a substitution at amino acid position 20 (D20) and a substitution at amino acid position 38 (R38) was tested in proliferation assays in both the NK-92 and TF1+ IL-2Rβ cell lines as described in Example 5 above. The modified hIL-2 proteins were grouped into 7 groups (1 to 7) based upon the maximal agonist activity of the modified hIL-2 protein and the level of attenuation of potency on both the intermediate and high-affinity receptors (Table 27) relative to non-modified recombinant hIL-2. The criteria used for grouping the modified hIL-2 proteins was:

Group 1: Variants with the highest attenuation (i.e., >10,000-fold) and at least about 80% activity on the intermediate-affinity receptor but also had high attenuation and at least about 70% activity on the high-affinity receptor.

Group 2: Variants with at least about 70% activity and >1,000-fold attenuation on the intermediate-affinity receptor, and about 20% activity to about 30% activity on the high-affinity receptor.

Group 3: Variants with about 50% activity to about 70% activity and >1,000-fold attenuation on the intermediate-affinity receptor, and about 20% activity on the high-affinity receptor.

Group 4: Variants with at least about 70% activity but only >500-fold attenuation on the intermediate-affinity receptor, and about 50% activity on the high-affinity receptor.

Group 5: Variants with at least about 70% activity on both receptors but >10-fold to >300-fold attenuation on the intermediate-affinity receptor in descending order and 70-fold to 1500-fold attenuation on the high-affinity receptor also in descending order.

Group 6: Variants with only about 30% activity and >2,500-fold attenuation on the intermediate-affinity receptor, and no activity on the high-affinity receptor.

Group 7: Variants with no activity on both the intermediate-affinity receptor and high-affinity receptor.

TABLE 27

Fold change from rhIL-2 and agonistic activity of modified hIL-2 proteins comprising a substitution at amino acid position 20 (D20) and a substitution at amino acid position 38 (R38) in a cell-based proliferation assay

	Variants	SEQ ID NO of hIL-2 variant	Fold change from rhIL-2 (NK-92)	Agonistic Activity (NK-92)	Fold change from rhIL-2 (TF1 + IL-2Rβ)	Agonistic Activity (TF1 + IL-2Rβ)
Group 1	1H3-hIgG1-L6-hIL-2 (D20A/R38E)	149	1183-2016	at least about 70%	>10,000 [a]	at least about 80%
Group 2	1H3-hIgG1-L6-hIL-2 (D20Q/R38E)	608	>10,000 [a]	about 30%	6665	at least about 70%
Group 2	1H3-hIgG1-L6-hIL-2 (D20M/R38E)	614	>10,000 [a]	about 30%	2607	at least about 70%
Group 2	1H3-hIgG1-L6-hIL-2 (D20I/R38E)	611	>10,000 [a]	about 20%	1782	at least about 70%
Group 3	1H3-hIgG1-L6-hIL-2 (D20V/R38E)	620	>10,000 on graph, NC [a]	about 20%	1849	about 50%
Group 4	1H3-hIgG1-L6-hIL-2 (D20S/R38E)	307	>10,000 on graph, NC [a]	about 50%	626	at least about 70%
Group 5	1H3-hIgG1-L6-hIL-2 (D20N/R38E)	607	1521	at least about 70%	378	at least about 70%
Group 5	1H3-hIgG1-L6-hIL-2 (D20G/R38E)	610	1288	at least about 70%	212	at least about 70%
Group 5	1H3-hIgG1-L6-hIL-2 (D20T/R38E)	617	524	at least about 70%	75	at least about 70%
Group 5	1H3-hIgG1-L6-hIL-2 (D20E/R38E)	609	77	at least about 70%	12	at least about 70%
Group 6	1H3-hIgG1-L6-hIL-2 (D20H/R38E)	306	No activity	No activity	2945	about 30%
Group 7	1H3-hIgG1-L6-hIL-2 (D20L/R38E)	612	>10,000 [a]	No activity	>10,000 [a]	No activity
Group 7	1H3-hIgG1-L6-hIL-2 (D20K/R38E)	613	No activity	No activity	544	No activity
Group 7	1H3-hIgG1-L6-hIL-2 (D20F/R38E)	615	>10,000 [a]	No activity	>10,000 [a]	No activity
Group 7	1H3-hIgG1-L6-hIL-2 (D20P/R38E)	616	>10,000 [a]	No activity	>10,000 [a]	No activity
Group 7	1H3-hIgG1-L6-hIL-2 (D20W/R38E)	618	>10,000 [a]	No activity	>10,000 [a]	No activity
Group 7	1H3-hIgG1-L6-hIL-2 (D20Y/R38E)	619	>10,000 [a]	No activity	1	No activity
Group 7	1H3-hIgG1-L6-hIL-2 (D20R/R38E)	606	>10,000 [a]	No activity	>10,000 [a]	No activity

Example 23: Activity of Surrogate Fusion Protein in a Murine MC38 Colo-Rectal Tumor Model

Ten week old female C57BL/6NCrl mice were injected into the right flank with 5×10^5 syngeneic MC38 colorectal carcinoma cells. When tumors reached 80-120 mm^3, mice were sorted into cohorts (10 mice/group) and treatment began on day 1 of study. All agents except hIL-2 were dosed intraperitoneally at 5 mg/kg twice weekly for 4 weeks, starting on day 1. hIL-2 was dosed intraperitoneally at 36,000 International Units once a day from days 1-5. Tumor size was measured with calipers twice weekly for the duration of the study. The study endpoint was a tumor volume of 1000 mm^3 or survival at day 50 or progression free survival at day 70, whichever came first.

All test agents including antibody molecules and antibody-hIL-2 fusion proteins were generated using a mouse IgG2b Fc region with a single N297A amino-acid substitution at position 297, which prevents glycosylation of the Fc region and significantly reduces any Fc region-mediated immune effector function, thereby preventing cellular depletion in vivo. Anti-mPD-1 RMP1-14 is a monoclonal antibody antagonist of the mouse PD-1 receptor (Matsumoto, J Immunol 172:2530-2541, 2004). Anti-mPD-1 RMP1-14-hIL-2 F42K/Y45R/V69R is a bi-functional fusion protein consisting of the monoclonal RMP1-14 antibody antagonist of the mouse PD-1 receptor fused at its C-terminus via a flexible six amino-acid glycine/serine linker to hIL-2 F42K/Y45R/V69R (SEQ ID NO: 621) that is a reduced potency IL-2 variant. This molecule was designed to target a reduced potency hIL-2 variant directly to PD-1 expressing T cells in vivo in mice. Anti-KLH-hIL-2 F42K, Y45R, V69R is a control fusion protein consisting of an isotype control monoclonal antibody recognizing a non-mammalian antigen (keyhole limpet hemocyanin, KLH) fused at its C-terminus via a flexible six amino-acid glycine/serine linker to hIL-2 F42K, Y45R, V69R that is a reduced potency IL-2 variant.

Results are presented in FIG. **19**. The MC38 colo-rectal tumor model is particularly responsive to antibody mediated PD-1 receptor inhibition. Although tumors growing in vehicle-treated mice rapidly reached study endpoint, 50% of mice treated with anti-mPD-1 RMP1-14 experienced complete tumor regression. In contrast, 100% of mice treated with an anti-mPD-1 RMP1-14-hIL-2 F42K, Y45R, V69R fusion protein experienced durable, long-term tumor regression. Mice treated with various combinations of the individual components of anti-mPD-1 RMP1-14-hIL-2 F42K, Y45R, V69R fusion protein, including either anti-mPD-1 RMP1-14 combined with hIL-2 free cytokine (administered at a dose and regimen equivalent to a therapeutic dose in humans) or anti-mPD-1 RMP1-14 combined with a non-targeted anti-KLH-hIL-2 F42K, Y45R, V69R fusion protein did not recapitulate the efficacy seen with anti-mPD-1 RMP1-14-hIL-2 F42K, Y45R, V69R. These data demonstrate that targeting a reduced potency hIL-2 to PD-1 expressing cells significantly improves anti-tumor efficacy relative to an anti-PD-1 receptor antagonist and that the activity of the fusion protein is not due to the additive effects of the molecule's individual components.

Example 24: Evaluation of Protective Anti-Tumor Immunity Induced by Surrogate Anti-mPD-1 RMP1-14-hIL-2 F42K, Y45R, V69R in the MC38 Colo-Rectal Tumor Model

Mice that had undergone a complete tumor regression in the primary tumor study described in Example 23 and that had survived to day 50 were subjected to a secondary tumor challenge without any additional drug therapy. For tumor re-challenge, mice were implanted on the left flank contralateral to the location of the primary tumor with 5×10^5 MC38 tumor cells. As a control group, 10 age-matched tumor naïve mice were also implanted with MC38 tumor cells.

FIG. **20** shows that all mice that had previously undergone a complete tumor regression in a prior primary tumor study and had survived to day 50 after treatment with anti-mPD-1 RMP1-14-hIL-2 F42K, Y45R, V69R were completely protected from secondary tumor development. In contrast, all tumor-naïve mice implanted with MC38 tumor cells went on to develop tumors that rapidly reached study endpoint of tumor volume of 100 mm^3. The development of protective anti-tumor immunity in the absence of continued drug therapy suggests that anti-mPD-1 RMP1-14-hIL-2 F42K, Y45R, V69R induced an anti-tumor memory T cell response.

Those skilled in the art will appreciate that numerous changes and modifications can be made to the preferred embodiments disclosed herein and that such changes and modifications can be made without departing from the spirit of the invention. It is, therefore, intended that the appended claims cover all such equivalent variations as fall within the true spirit and scope of the invention.

The disclosures of each patent, patent application, and publication cited or described in this document are hereby incorporated herein by reference, in its entirety.

TABLE 28

Exemplary Antibodies

Antibody Name	Heavy chain	Light chain
Anti-hPD-1 #1-mIgG2b-N297A	Anti-hPD-1 #1-mIgG2b-N297A HC (SEQ ID NO: 348)	Anti-hPD-1 #1-mKappa LC (SEQ ID NO: 349)
Anti-hPD-1 #2-mIgG2b-N297A	Anti-hPD-1 #2-mIgG2b-N297A HC (SEQ ID NO: 350)	Anti-hPD-1 #2-mKappa LC (SEQ ID NO: 351)
hIL-2 Nterm light chain df	1H3-hIgG1 HC (SEQ ID NO: 379)	hIL-2-df-1H3-hkappa LC (SEQ ID NO: 356)
hIL-2 Nterm light chain L6 fusion	1H3-hIgG1 HC (SEQ ID NO: 379)	hIL-2-L6-1H3-hkappa LC (SEQ ID NO: 357)
hIL-2 Nterm heavy chain df	hIL-2-df-1H3-hIgG1 HC (SEQ ID NO: 358)	1H3-hKappa LC (SEQ ID NO: 374)
hIL-2 Nterm heavy chain L6 fusion	hIL-2-L6-1H3-hIgG1 HC (SEQ ID NO: 359)	1H3-hKappa LC (SEQ ID NO: 374)
hIL-2 Cterm heavy chain df	1H3-hIgG1-df-hIL-2 HC (SEQ ID NO: 360)	1H3-hKappa LC (SEQ ID NO: 374)
hIL-2 Cterm heavy chain L6 fusion	1H3-hIgG1-L6-hIL-2 HC (SEQ ID NO: 361)	1H3-hKappa LC (SEQ ID NO: 374)

TABLE 28-continued

Exemplary Antibodies

Antibody Name	Heavy chain	Light chain
hIL-2 Cterm light chain df	1H3-hIgG1 HC (SEQ ID NO: 379)	1H3-hKappa-df-hIL-2 (WT) LC (SEQ ID NO: 362)
hIL-2 Cterm light chain L6 fusion	1H3-hIgG1 HC (SEQ ID NO: 379)	1H3-hKappa-L6-hIL-2 (WT) LC (SEQ ID NO: 363)
hCD25-L20-hIL-2 Nterm heavy chain df	hCD25-L20-hIL-2-df-1H3-hIgG1 HC (SEQ ID NO: 365)	1H3-hKappa LC (SEQ ID NO: 374)
hCD25-L20-hIL-2 Nterm heavy chain L6 fusion	hCD25-L20-hIL-2-L6-1H3-hIgG1 HC (SEQ ID NO: 366)	1H3-hKappa LC (SEQ ID NO: 374)
hCD25-L20-hIL-2 Nterm light chain df	1H3-hIgG1 HC (SEQ ID NO: 379)	hCD25-L20-hIL-2-df-1H3-hKappa LC (SEQ ID NO: 367)
hCD25-L20-hIL-2 Nterm light chain L6 fusion	1H3-hIgG1 HC (SEQ ID NO: 379)	hCD25-L20-hIL-2-L6-1H3-hKappa LC (SEQ ID NO: 368)
hCD25-L20-hIL-2 Cterm heavy chain df	1H3-hIgG1-df-hCD25-L20-hIL-2 HC (SEQ ID NO: 369)	1H3-hKappa LC (SEQ ID NO: 374)
hCD25-L20-hIL-2 Cterm heavy chain L6 fusion	1H3-hIgG1-L6-hCD25-L20-hIL-2 HC (SEQ ID NO: 370)	1H3-hKappa LC (SEQ ID NO: 374)
hCD25-L20-hIL-2 Cterm light chain df	1H3-hIgG1 HC (SEQ ID NO: 379)	1H3-hKappa-df-hCD25-L20-hIL-2 LC (SEQ ID NO: 371)
hCD25-L20-hIL-2 Cterm light chain L6 fusion	1H3-hIgG1 HC (SEQ ID NO: 379)	1H3-hKappa-L6-hCD25-L20-hIL-2 LC (SEQ ID NO: 372)
2D12-mIgG1-D265A-L6-hIL-2	2D12-mIgG1-D265A-L6-hIL-2 HC (SEQ ID NO: 375)	2D12-mKappa LC (SEQ ID NO: 376)
2H7-hIgG4	2H7-hIgG4 HC (SEQ ID NO: 424)	2H7-hKappa LC (SEQ ID NO: 425)
C51E6-5-hIgG4	C51E6-5-hIgG4 HC (SEQ ID NO: 426)	C51E6-5-hKappa LC (SEQ ID NO: 427)
A2-hIgG4	A2-hIgG4 HC (SEQ ID NO: 428)	A2-hLambda LC (SEQ ID NO: 429)
H7-632-hIgG1-LAGA	H7-632 HC (SEQ ID NO: 414)	H7-632 LC (SEQ ID NO: 415)
2H7-hIgG4-df-hIL-2 (D20A/R38E)	2H7-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 430)	2H7-hKappa LC (SEQ ID NO: 425)
C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E)	C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E) HC (SEQ ID NO: 432)	C51E6-5-hKappa LC (SEQ ID NO: 427)
A2-hIgG4-df-hIL-2 (D20A/R38E)	A2-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 433)	A2-hLambda LC (SEQ ID NO: 429)
1H3-hIgG4-df-hIL-2 (D20A/R38E)	1H3-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 434)	1H3-hKappa LC (SEQ ID NO: 374)
2H7-hIgG4-df-hIL-2 (T3A/D20A/R38E/C125A)	2H7-hIgG4-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 435)	2H7-hKappa LC (SEQ ID NO: 425)
OMC.1.B6-hIgG4	OMC.1.B6-hIgG4 HC (SEQ ID NO: 438)	OMC.1.B6-hLambda LC (SEQ ID NO: 439)
OMC.2.C6-hIgG4	OMC.2.C6-hIgG4 HC (SEQ ID NO: 440)	OMC.2.C6-hLambda LC (SEQ ID NO: 441)
OMC.1.D6-hIgG4	OMC.1.D6-hIgG4 HC (SEQ ID NO: 442)	OMC.1.D6-hLambda LC (SEQ ID NO: 443)
D12-hIgG4	D12-hIgG4 HC (SEQ ID NO: 444)	D12-hLambda LC (SEQ ID NO: 445)
G12-hIgG4	G12-hIgG4 HC (SEQ ID NO: 446)	G12-hLambda LC (SEQ ID NO: 447)
Abz1mod-hIgG4	Abz1mod-hIgG4 HC (SEQ ID NO: 449)	Abz1mod-hKappa LC (SEQ ID NO: 450)
Anti-hPD-1 #1-hIgG4-L6-hIL-2 (D20A/R38E)	Anti-hPD-1 #1-hIgG4-L6-hIL-2 (D20A/R38E) (SEQ ID NO: 451)	Anti-hPD-1 #1-hKappa (SEQ ID NO: 452)
OMC.1.B6-hIgG4-L6-hIL-2 (D20A/R38E)	OMC.1.B6-hIgG4-L6-hIL-2 (D20A/R38E) HC (SEQ ID NO: 453)	OMC.1.B6-hLambda LC (SEQ ID NO: 439)
OMC.2.C6-hIgG4-L6-hIL-2 (D20A/R38E)	OMC.2.C6-hIgG4-L6-hIL-2 (D20A/R38E) HC (SEQ ID NO: 454)	OMC.2.C6-hLambda LC (SEQ ID NO: 441)
OMC.1.D6-hIgG4-L6-hIL-2 (D20A/R38E)	OMC.1.D6-hIgG4-L6-hIL-2 (D20A/R38E) HC (SEQ ID NO: 455)	OMC.1.D6-hLambda LC (SEQ ID NO: 443)
D12-hIgG4-df-hIL-2 (D20A/R38E)	D12-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 456)	D12-hLambda LC (SEQ ID NO: 445)
G12-hIgG4-df-hIL-2 (D20A/R38E)	G12-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 457)	G12-hLambda LC (SEQ ID NO: 447)
2H7-hIgG4-LE	2H7-hIgG4-LE HC (SEQ ID NO: 458)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG4-LAGA	2H7-hIgG4-LAGA HC (SEQ ID NO: 459)	2H7-hKappa LC (SEQ ID NO: 425)
OMC476pH7-hIgG4	OMC476pH7-hIgG4 HC (SEQ ID NO: 461)	OMC476pB11.H7 LC (SEQ ID NO: 462)
OMC476pB11-hIgG4	OMC476pB11-hIgG4 HC (SEQ ID NO: 463)	OMC476pB11.H7 LC (SEQ ID NO: 462)
OMC476pG10-hIgG4	OMC476pG10-hIgG4 HC (SEQ ID NO: 464)	OMC476pG10.H10 LC (SEQ ID NO: 466)
OMC476pH10-hIgG4	OMC476pH10-hIgG4 HC (SEQ ID NO: 465)	OMC476pG10.H10 LC (SEQ ID NO: 466)
OMC476pE4-hIgG4	OMC476pE4-hIgG4 HC (SEQ ID NO: 467)	OMC476pE4 LC (SEQ ID NO: 468)
J110-hIgG1	J110-hIgG1 HC (SEQ ID NO: 469)	J110-hKappa LC (SEQ ID NO: 470)
2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 471)	2H7-hKappa LC (SEQ ID NO: 425)

TABLE 28-continued

Exemplary Antibodies

Antibody Name	Heavy chain	Light chain
2H7-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	2H7-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 472)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	2H7-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 473)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A)	2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A) HC (SEQ ID NO: 474)	2H7-hKappa LC (SEQ ID NO: 425)
hIgG4-LE-df-hIL-2 (T3A/R38E/I92K/C125A)	hIgG4-LE-df-hIL-2 (T3A/R38E/I92K/C125A) HC (SEQ ID NO: 475)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A)	2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A) HC (SEQ ID NO: 476)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A)	2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A) HC (SEQ ID NO: 477)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/D84K/C125A)	2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/D84K/C125A) HC (SEQ ID NO: 478)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A)	2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A) HC (SEQ ID NO: 479)	2H7-hKappa LC (SEQ ID NO: 425)
1H3-hIgG4-df-hIL-2 (WT)	1H3-hIgG4-df-hIL-2 (WT) HC (SEQ ID NO: 480)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (WT)	1H3-hIgG4-L6-hIL-2 (WT) HC (SEQ ID NO: 481)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-df-hIL-2 (WT) LC fusion	1H3-hIgG4 HC (SEQ ID NO: 482)	1H3-hKappa-df-hIL-2 (WT) LC (SEQ ID NO: 362)
1H3-hIgG4-L6-hIL-2 (WT) LC fusion	1H3-hIgG4 HC (SEQ ID NO: 482)	1H3-hKappa-L6-hIL-2 (WT) LC (SEQ ID NO: 363)
1H3-hIgG4-L6-hIL-2 (D20Y)	1H3-hIgG4-L6-hIL-2 (D20Y) HC (SEQ ID NO: 485)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-df-hIL-2 (D20Y)	1H3-hIgG4-df-hIL-2 (D20Y) HC (SEQ ID NO: 486)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG1-df-hIL-2 (D20Y)	1H3-hIgG1-df-hIL-2 (D20Y) HC (SEQ ID NO: 487)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (D20A/R38P)	1H3-hIgG4-L6-hIL-2 (D20A/R38P) HC (SEQ ID NO: 488)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (D20A/R38S)	1H3-hIgG4-L6-hIL-2 (D20A/R38S) HC (SEQ ID NO: 489)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (D20A/R38D)	1H3-hIgG4-L6-hIL-2 (D20A/R38D) HC (SEQ ID NO: 490)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (D20A/R38Q/E95A)	1H3-hIgG4-L6-hIL-2 (D20A/R38Q/E95A) HC (SEQ ID NO: 491)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (D20A/F42H/E95A)	1H3-hIgG4-L6-hIL-2 (D20A/F42H/E95A) HC (SEQ ID NO: 492)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (R38D/I92D)	1H3-hIgG4-L6-hIL-2 (R38D/I92D) HC (SEQ ID NO: 493)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (R38E/I92D)	1H3-hIgG4-L6-hIL-2 (R38E/I92D) HC (SEQ ID NO: 494)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (F42H/I92D)	1H3-hIgG4-L6-hIL-2 (F42H/I92D) HC (SEQ ID NO: 495)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (D20A/R38E)	1H3-hIgG4-L6-hIL-2 (D20A/R38E) HC (SEQ ID NO: 496)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (T3A/D20A/R38E)	1H3-hIgG4-L6-hIL-2 (T3A/D20A/R38E) HC (SEQ ID NO: 497)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (D20A/R38E/C125A)	1H3-hIgG4-L6-hIL-2 (D20A/R38E/C125A) HC (SEQ ID NO: 498)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-L6-hIL-2 (T3A/D20A/R38E/C125A)	1H3-hIgG4-L6-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 499)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hIL-2 (D20A/R38E)	1H3-hIgG1-L6-hIL-2 (D20A/R38E) HC (SEQ ID NO: 500)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E)	1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E) HC (SEQ ID NO: 501)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hIL-2 (D20A/R38E/C125A)	1H3-hIgG1-L6-hIL-2 (D20A/R38E/C125A) HC (SEQ ID NO: 502)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG4-df-hIL-2 (D20A/R38E) LC fusion	1H3-hIgG4 HC (SEQ ID NO: 482)	1H3-hKappa-df-hIL-2 (D20A/R38E) LC (SEQ ID NO: 503)

TABLE 28-continued

Exemplary Antibodies

Antibody Name	Heavy chain	Light chain
1H3-hIgG4-L6-hIL-2 (D20A/R38E) LC fusion	1H3-hIgG4 HC (SEQ ID NO: 482)	1H3-hKappa-L6-hIL-2 (D20A/R38E) LC (SEQ ID NO: 504)
OMC476pB11-hIgG4-df-hIL-2 (D20A/R38E)	OMC476pB11-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 505)	OMC476pB11.H7 LC (SEQ ID NO: 462)
OMC476pE4-hIgG4-df-hIL-2 (D20A/R38E)	OMC476pE4-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 506)	OMC476pE4 LC (SEQ ID NO: 468)
OMC476pG10-hIgG4-df-hIL-2 (D20A/R38E)	OMC476pG10-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 507)	OMC476pG10.H10 LC (SEQ ID NO: 466)
OMC476pH10-hIgG4-df-hIL-2 (D20A/R38E)	OMC476pH10-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 508)	OMC476pG10.H10 LC (SEQ ID NO: 466)
A2-hIgG4-df-hIL-2 (D20A/F42A)	A2-hIgG4-df-hIL-2 (D20A/F42A) HC (SEQ ID NO: 509)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4-df-hIL-2 (D20A/F42S)	A2-hIgG4-df-hIL-2 (D20A/F42S) HC (SEQ ID NO: 510)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4-df-hIL-2 (D20S/R38E)	A2-hIgG4-df-hIL-2 (D20S/R38E) HC (SEQ ID NO: 511)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4-df-hIL-2 (F42A/N88R)	A2-hIgG4-df-hIL-2 (F42A/N88R) HC (SEQ ID NO: 512)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4-df-hIL-2 (F42I/I92D)	A2-hIgG4-df-hIL-2 (F421/I92D) HC (SEQ ID NO: 513)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4-df-hIL-2 (F42Q/I92D)	A2-hIgG4-df-hIL-2 (F42Q/I92D) HC (SEQ ID NO: 514)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4-df-hIL-2 (F42T/I92D)	A2-hIgG4-df-hIL-2 (F42T/I92D) HC (SEQ ID NO: 515)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4-df-hIL-2 (F42W/I92D)	A2-hIgG4-df-hIL-2 (F42W/I92D) HC (SEQ ID NO: 516)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4-df-hIL-2 (R38E/D84K)	A2-hIgG4-df-hIL-2 (R38E/D84K) HC (SEQ ID NO: 517)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4-df-hIL-2 (R38E/I92K)	A2-hIgG4-df-hIL-2 (R38E/I92K) HC (SEQ ID NO: 518)	A2-hLambda LC (SEQ ID NO: 429)
C51E6-5-hIgG4-df-hIL-2 (D20A/R38E)	C51E6-5-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 519)	C51E6-5-hKappa LC (SEQ ID NO: 427)
C51E6-5-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	C51E6-5-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 520)	C51E6-5-hKappa LC (SEQ ID NO: 427)
C51E6-5-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	C51E6-5-hIgG4-LAGA-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 521)	C51E6-5-hKappa LC (SEQ ID NO: 427)
2A3.H7-hIgG4-df-hIL-2 (D20A/R38E)	2H7-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 430)	2A3-hKappa LC (SEQ ID NO: 523)
1H9-hIgG4-df-hIL-2 (D20A/R38E)	1H9-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 524)	1H9-hKappa LC (SEQ ID NO: 525)
1D5-hIgG4-df-hIL-2 (D20A/R38E)	1D5-hIgG4-df-hIL-2 (D20A/R38E) HC (SEQ ID NO: 526)	1D5-hKappa LC (SEQ ID NO: 527)
1D5-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	1D5-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 528)	1D5-hKappa LC (SEQ ID NO: 527)
1D5-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	1D5-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 529)	1D5-hKappa LC (SEQ ID NO: 527)
2H7-hIgG1-df-hIL-2 (T3A/D20A/R38E/C125A)	2H7-hIgG1-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 530)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	2H7-hIgG1-LE-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 531)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LE-df-hIL-2 (T3A/R38E/D84K/C125A)	2H7-hIgG1-LE-df-hIL-2 (T3A/R38E/D84K/C125A) HC (SEQ ID NO: 533)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG4-df-hIL-2 (T3A/R38E/D84K/C125A)	2H7-hIgG4-df-hIL-2 (T3A/R38E/D84K/C125A) HC (SEQ ID NO: 534)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-df-hIL-2 (T3A/R38E/I92K/C125A)	2H7-hIgG1-df-hIL-2 (T3A/R38E/I92K/C125A) HC (SEQ ID NO: 535)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LE-df-hIL-2 (T3A/R38E/I92K/C125A)	2H7-hIgG1-LE-df-hIL-2 (T3A/R38E/I92K/C125A) HC (SEQ ID NO: 536)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG4-df-hIL-2 (T3A/R38E/I92K/C125A)	2H7-hIgG4-df-hIL-2 (T3A/R38E/I92K/C125A) HC (SEQ ID NO: 537)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LAGA-df-hIL2 (T3A/D20S/R38E/C125A)	2H7-hIgG1-LAGA-df-hIL2 (T3A/D20S/R38E/C125A) HC (SEQ ID NO: 538)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/D84F/C125A)	2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/D84F/C125A) HC (SEQ ID NO: 539)	2H7-hKappa LC (SEQ ID NO: 425)

TABLE 28-continued

Exemplary Antibodies

Antibody Name	Heavy chain	Light chain
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192R/C125A)	2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192R/C125A) HC (SEQ ID NO: 540)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192E/C125A)	2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192E/C125A) HC (SEQ ID NO: 541)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192S/C125A)	2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192S/C125A) HC (SEQ ID NO: 542)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/I92D/C125A)	2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/I92D/C125A) HC (SEQ ID NO: 543)	2H7-hKappa LC (SEQ ID NO: 425)
2H7-hIgG1-LAGA-df-hIL2 (T3A/H16E/R38E/C125A)	2H7-hIgG1-LAGA-df-hIL2 (T3A/H16E/R38E/C125A) HC (SEQ ID NO: 544)	2H7-hKappa LC (SEQ ID NO: 425)
1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E/C125A)	1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 545)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 546)	1H3-hKappa LC (SEQ ID NO: 374)
C51E6-5-hIgG4/k-LE	C51E6-5-hIgG4/k-LE HC (SEQ ID NO: 547)	C51E6-5-hKappa LC (SEQ ID NO: 427)
C51E6-5-hIgG4/k-LAGA	C51E6-5-hIgG4/k-LAGA HC (SEQ ID NO: 548)	C51E6-5-hKappa LC (SEQ ID NO: 427)
C51E6-5-hIgG4/k-LEPG	C51E6-5-hIgG4/k-LEPG HC (SEQ ID NO: 549)	C51E6-5-hKappa LC (SEQ ID NO: 427)
C51E6-5-hIgG4/k-df-hIL-2 (T3A/D20A/R38E/C125A)	C51E6-5-hIgG4/k-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 550)	C51E6-5-hKappa LC (SEQ ID NO: 427)
C51E6-5-hIgG4/k-LEPG-hIL-2 (T3A/D20A/R38E/C125A)	C51E6-5-hIgG4/k-LEPG-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 551)	C51E6-5-hKappa LC (SEQ ID NO: 427)
A2-hIgG4/k-LE	A2-hIgG4/k-LE HC (SEQ ID NO: 552)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4/k-LAGA	A2-hIgG4/k-LAGA HC (SEQ ID NO: 553)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4/k-LEPG	A2-hIgG4/k-LEPG HC (SEQ ID NO: 554)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4/k-df-hIL-2 (T3A/D20A/R38E/C125A)	A2-hIgG4/k-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 555)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4/k-LE-df-hIL-2 (T3A/D20A/R38E/C125A)	A2-hIgG4/k-LE-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 556)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4/k-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	A2-hIgG4/k-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 557)	A2-hLambda LC (SEQ ID NO: 429)
A2-hIgG4/k-LEPG-df-hIL-2 (T3A/D20A/R38E/C125A)	A2-hIgG4/k-LEPG-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 558)	A2-hLambda LC (SEQ ID NO: 429)
Anti-CD20-hIgG1/k	Anti-CD20-hIgG1/k HC (SEQ ID NO: 560)	Anti-CD20-hKappa LC (SEQ ID NO: 562)
Anti-CD20-hIgG1/k-LAGA	Anti-CD20-hIgG1/k-LAGA HC (SEQ ID NO: 561)	Anti-CD20-hKappa LC (SEQ ID NO: 562)
1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A)	1H3-hIgG1-LAGA-df-hIL-2 T3A/C125A) HC (SEQ ID NO: 563)	1H3-hKappa LC (SEQ ID NO: 374)
anti-mPD-1 RMP1-14 mIgG2b-N297A	anti-mPD-1 RMP1-14 mIgG2b-N297A HC (SEQ ID NO: 564)	anti-mPD-1 RMP1-14 mKappa LC (SEQ ID NO: 566)
anti-mPD-1 RMP1-14 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)	anti-mPD-1 RMP1-14 mIgG2b-N297A-L6-hIL-2(F42K/Y45R/V69R) HC (SEQ ID NO: 565)	anti-mPD-1 RMP1-14 mKappa LC (SEQ ID NO: 566)
anti-mPD-1 RMP1-30 mIgG2b-N297A	anti-mPD-1 RMP1-30 mIgG2b-N297A HC (SEQ ID NO: 567)	anti-mPD-1 RMP1-30 mKappa LC (SEQ ID NO: 568)
anti-mPD-1 RMP1-30 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)	anti-mPD-1 RMP1-30 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) HC (SEQ ID NO: 569)	anti-mPD-1 RMP1-30 mKappa LC (SEQ ID NO: 568)
anti-KLH-C3-mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R)	anti-KLH-C3-mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) HC (SEQ ID NO: 570)	KLH-C3-mKappa LC (SEQ ID NO: 571)
2D12-hIgG1-L6-hIL-2	2D12-hIgG1-L6-hIL-2 HC (SEQ ID NO: 572)	2D12-hKappa LC (SEQ ID NO: 573)

TABLE 28-continued

Exemplary Antibodies

Antibody Name	Heavy chain	Light chain
1H9-hIgG4	1H9-hIgG4 HC (SEQ ID NO: 576)	1H9-hKappa LC (SEQ ID NO: 525)
1D5-hIgG4	1D5-hIgG4 HC (SEQ ID NO: 577)	1D5-hKappa LC (SEQ ID NO: 527)
2A3.H7-hIgG4	2H7-hIgG4 HC (SEQ ID NO: 424)	2A3-hKappa LC (SEQ ID NO: 523)
H7-02-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A)	H7-02-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC (SEQ ID NO: 582)	H7-02-hKappa LC (SEQ ID NO: 583)
KLH-C3-hIgG4	KLH-C3-hIgG4 HC (SEQ ID NO: 585)	KLH-C3-hKappa LC (SEQ ID NO: 586)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E15A)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E15A) HC (SEQ ID NO: 587)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20I)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D201) HC (SEQ ID NO: 588)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20S)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20S) HC (SEQ ID NO: 589)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20H)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20H) HC (SEQ ID NO: 590)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20W)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20W) HC (SEQ ID NO: 591)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20Y)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20Y) HC (SEQ ID NO: 592)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20R)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20R) HC (SEQ ID NO: 593)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20F)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D20F) HC (SEQ ID NO: 594)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D84K)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (D84K) HC (SEQ ID NO: 595)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (S87A)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (S87A) HC (SEQ ID NO: 596)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88Y)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88Y) HC (SEQ ID NO: 597)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88D)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88D) HC (SEQ ID NO: 598)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88R)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88R) HC (SEQ ID NO: 599)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88E)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88E) HC (SEQ ID NO: 600)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88F)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88F) HC (SEQ ID NO: 601)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88I)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (N88I) HC (SEQ ID NO: 602)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (I92A)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (I92A) HC (SEQ ID NO: 603)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E95A)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E95A) HC (SEQ ID NO: 604)	1H3-hkappa LC (SEQ ID NO: 374)
1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E95K)	1H3-hIgG1-L6-hCD25(1-164)-L20-hIL-2 (E95K) HC (SEQ ID NO: 605)	1H3-hkappa LC (SEQ ID NO: 374)
H7-02-hIgG4	H7-02-hIgG4 HC (SEQ ID NO: 373)	H7-02 hKappa LC (SEQ ID NO: 607)
H7-632-hIgG1-LAGA-df-hIL-2 (T3A/C125A)	H7-632-hIgG1-LAGA-df-hIL-2 (T3A/C125A) HC (SEQ ID NO: 431)	H7-632 LC (SEQ ID NO: 415)
1H3-hIgG1-LAGA-L6-hIL-2 (T3A/D20A/R38E/C125A)	1H3-hIgG1-LAGA-L6-hIL-2 (T3A/D20A/R38E/C125A) (SEQ ID NO: 522)	1H3-hKappa LC (SEQ ID NO: 374)
1H3-hIgG1	1H3-hIgG1 HC (SEQ ID NO: 379)	1H3-hKappa LC (SEQ ID NO: 374)
H7-767	H7-767 HC (SEQ ID NO: 532)	H7-632 LC (SEQ ID NO: 415)
Anti-hPD-1 #1	Anti-hPD-1 #1 HC (SEQ ID NO: 559)	Anti-hPD-1#1-hKappa (SEQ ID NO: 452)
Anti-hPD-1 #2	Anti-hPD-1 #2 HC (SEQ ID NO: 578)	Anti-hPD-1 #2 LC (SEQ ID NO: 579)
2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/I92K/C125A)	2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/I92K/C125A) HC (SEQ ID NO: 475)	2H7-hKappa LC (SEQ ID NO: 425)

TABLE 29

Sequences

SEQ ID NO:	Name	Sequence
1	hIL-2 F42K	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**K**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
2	hIL-2 V69A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**A** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
3	hIL-2 V69E	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**E** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
4	hIL-2 V69F	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**F** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
5	hIL-2 V69G	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**G** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
6	hIL-2 V69H	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**H** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
7	hIL-2 V69I	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**I** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
8	hIL-2 V69K	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**K** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
9	hIL-2 V69L	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**L** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
10	hIL-2 V69M	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**M** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
11	hIL-2 V69Q	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**Q** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
12	hIL-2 V69S	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**S** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
13	hIL-2 V69T	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**T** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
14	hIL-2 V69W	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**W** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
15	hIL-2 V69Y	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**Y** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
16	hIL-2 F42K/F44K	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**KK**YMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
17	hIL-2 F44K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFK**KR**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
18	hIL-2 F42K/V69R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKFYMPKKATELKHLQCLEEELKPLEER LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
19	hIL-2 Y45R/V69R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFRMPKKATELKHLQCLEEELKPLEER LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
20	hIL-2 F42K/F44K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKKRMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
21	hIL-2 R38A/F42K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTKKERMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
22	hIL-2 R38E/F42K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTEMLTKKERMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
23	hIL-2 K43E/F42K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKEFRMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
24	hIL-2 K43T/F42K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKTERMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
25	hIL-2 F42K/Y45R/E62A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKERMPKKATELKHLQCLEEALKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
26	hIL-2 P65R/F42K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKERMPKKATELKHLQCLEEELKRLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
27	hIL-2 P65S/F42K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKFRMPKKATELKHLQCLEEELKSLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
28	hIL-2 V69A/F42K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKERMPKKATELKHLQCLEEELKPLEEA LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
29	hIL-2 V69D/F42K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKERMPKKATELKHLQCLEEELKPLEED LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
30	hIL-2 V69R/F42K/Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKERMPKKATELKHLQCLEEELKPLEER LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
31	hIL-2 D20A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
32	hIL-2 D20N	APTSSSTKKTQLQLEHLLL**N**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
33	hIL-2 D20K	APTSSSTKKTQLQLEHLLL**K**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
34	hIL-2 N88A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**A**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
35	hIL-2 N88G	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**G**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
36	hIL-2 N88H	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**H**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
37	hIL-2 N88K	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**K**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
38	hIL-2 D20A/D84A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPR**A**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
39	hIL-2 D20A/E15A	APTSSSTKKTQLQL**A**HLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
40	hIL-2 D20A/E95A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
41	hIL-2 D20A/N88A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**A**INVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
42	hIL-2 D20A/S87A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIA**N**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
43	hIL-2 D84A/N88A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPR**A**LIS**A**INVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
44	hIL-2 E15A/N88A	APTSSSTKKTQLQL**A**HLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**A**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
45	hIL-2 S87A/N88A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLI**AA**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
46	hIL-2 R38A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**A**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
47	hIL-2 R38D	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**D**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
48	hIL-2 R38E	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
49	hIL-2 R38Q	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**Q**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
50	hIL-2 F42R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**R**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
51	hIL-2 F42A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**A**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
52	hIL-2 F42D	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**D**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
53	hIL-2 F42H	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**H**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
54	hIL-2 K43A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTF**A**FYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
55	hIL-2 K43E	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTF**E**FYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
56	hIL-2 K43Q	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTF**Q**FYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
57	hIL-2 Y45A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**A**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
58	hIL-2 Y45K	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**K**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
59	hIL-2 Y45S	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**S**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
60	hIL-2 Y45R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**R**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
61	hIL-2 E61A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL**A**AELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
62	hIL-2 E61R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL**R**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
63	hIL-2 E61K	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL**K**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
64	hIL-2 E62A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEE**A**LKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
65	hIL-2 E62R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEE**R**LKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
66	hIL-2 E62K	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEE**K**LKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
67	hIL-2 E62Y	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEE**Y**LKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
68	hIL-2 E68Y	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLE**Y**V LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
69	hIL-2 E68A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLE**A**V LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
70	hIL-2 E68K	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLE**K**V LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
71	hIL-2 E68R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLE**R**V LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
72	hIL-2 E68L	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLE**L**V LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
73	hIL-2 L72Y	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LN**Y**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
74	hIL-2 L72R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LN**R**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
75	hIL-2 L72A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LN**A**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
76	hIL-2 L72D	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LN**D**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
77	hIL-2 L72H	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LN**H**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
78	hIL-2 L72F	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LN**F**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
79	hIL-2 R38D/E61R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**D**MLTFKFYMPKKATELKHLQCL**E**R**R**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
80	hIL-2 R38D/E61R/K43E	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**D**MLTF**E**FYMPKKATELKHLQCL**E**R**R**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
81	hIL-2 T3A/F42A/Y45A/ L72G/C125A	AP**A**SSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**A**KF**A**MPKKATELKHLQCLEEELKPLEEV LN**G**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITF**A**QSIISTLT
82	hIL-2 E15A	APTSSSTKKTQLQL**A**HLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
83	hIL-2 E15R	APTSSSTKKTQLQL**R**HLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
84	hIL-2 E15K	APTSSSTKKTQLQL**K**HLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
85	hIL-2 H16A	APTSSSTKKTQLQLE**A**LLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
86	hIL-2 H16Y	APTSSSTKKTQLQLE**Y**LLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
87	hIL-2 H16E	APTSSSTKKTQLQLE**E**LLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
88	hIL-2 L19A	APTSSSTKKTQLQLEHLL**A**DLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
89	hIL-2 D20I	APTSSSTKKTQLQLEHLLL**I**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
90	hIL-2 D20S	APTSSSTKKTQLQLEHLLL**S**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
91	hIL-2 D20H	APTSSSTKKTQLQLEHLLL**H**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
92	hIL-2 D20T	APTSSSTKKTQLQLEHLLL**T**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
93	hIL-2 D20W	APTSSSTKKTQLQLEHLLL**W**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
94	hIL-2 D20Y	APTSSSTKKTQLQLEHLLL**Y**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
95	hIL-2 D20R	APTSSSTKKTQLQLEHLLL**R**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
96	hIL-2 D20F	APTSSSTKKTQLQLEHLLL**F**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
97	hIL-2 R81A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHL**A**PRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
98	hIL-2 D84A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPR**A**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
99	hIL-2 D84R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPR**R**LISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
100	hIL-2 D84K	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPR**K**LISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
101	hIL-2 S87A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLI**A**NINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
102	hIL-2 N88Y	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**Y**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
103	hIL-2 N88D	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**D**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
104	hIL-2 N88R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**R**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
105	hIL-2 N88E	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**E**INVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
106	hIL-2 N88F	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**F**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
107	hIL-2 N88I	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIS**I**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
108	hIL-2 I92A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**A**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
109	hIL-2 I92Y	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**Y**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
110	hIL-2 I92S	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**S**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
111	hIL-2 I92F	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**F**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
112	hIL-2 I92R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**R**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
113	hIL-2 I92D	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
114	hIL-2 I92E	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**E**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
115	hIL-2 E95A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
116	hIL-2 E95R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**R**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
117	hIL-2 E95K	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**K**LKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
118	hIL-2 D20Y/H16E	APTSSSTKKTQLQL**E**ELLL**Y**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
119	hIL-2 D20Y/H16A	APTSSSTKKTQLQLE**A**LLL**Y**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
120	hIL-2 D20Y/H16Y	APTSSSTKKTQLQLE**Y**LLL**Y**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
121	hIL-2 D20Y/I92A	APTSSSTKKTQLQLEHLLL**Y**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**A**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
122	hIL-2 D20Y/I92S	APTSSSTKKTQLQLEHLLL**Y**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**S**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
123	hIL-2 D20Y/I92R	APTSSSTKKTQLQLEHLLL**Y**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**R**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
124	hIL-2 D20Y/E95R	APTSSSTKKTQLQLEHLLL**Y**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**R**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
125	hIL-2 D20Y/E95A	APTSSSTKKTQLQLEHLLL**Y**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
126	hCD25 (1-164)	ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGERRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNT TKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRAL HRGPAESVCKMTHGKTRWTQPQLICT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
127	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTDKFYMPKKATELKHLQCLEEELKPLEEV
	F42D/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
128	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTRKFYMPKKATELKHLQCLEEELKPLEEV
	F42R/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
129	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTKKFYMPKKATELKHLQCLEEELKPLEEV
	F42K/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
130	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTAKFYMPKKATELKHLQCLEEELKPLEEV
	F42A/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
131	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTHKFYMPKKATELKHLQCLEEELKPLEEV
	F42H/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
132	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFRMPKKATELKHLQCLEEELKPLEEV
	Y45R/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
133	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFKMPKKATELKHLQCLEEELKPLEEV
	Y45K/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
134	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTNMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38N/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
135	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTGMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38G/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
136	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTHMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38H/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
137	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTIMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38I/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
138	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTLMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38L/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
139	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTMMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38M/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
140	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTFMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38F/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
141	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTPMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38P/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
142	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTSMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38S/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
143	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTTMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38T/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
144	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTWMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38W/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
145	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTYMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38Y/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
146	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTVMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38V/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
147	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTAMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38A/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
148	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTQMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38Q/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
149	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	D20A/R38E	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
150	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTDMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38D/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
151	hIL-2	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFEFYMPKKATELKHLQCLEEELKPLEEV
	K43E/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
152	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**A**ELKPLEEV
	E61A/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
153	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEE**A**LKPLEEV
	E62A/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
154	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEE**Y**LKPLEEV
	E62Y/D20A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
155	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	L72D/D20A	LN**D**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
156	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	L72H/D20A	LN**H**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
157	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	L72R/D20A	LN**R**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
158	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**D**KFYMPKKATELKHLQCLEEELKPLEEV
	F42D/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
159	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**R**KFYMPKKATELKHLQCLEEELKPLEEV
	F42R/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
160	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**H**KFYMPKKATELKHLQCLEEELKPLEEV
	F42H/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
161	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**A**KFYMPKKATELKHLQCLEEELKPLEEV
	F42A/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
162	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTF**E**FYMPKKATELKHLQCLEEELKPLEEV
	K43E/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
163	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**R**MPKKATELKHLQCLEEELKPLEEV
	Y45R/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
164	hIL-2 Y45K/I92	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**K**MPKKATELKHLQCLEEELKPLEEV
		LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
165	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEE**A**LKPLEEV
	E62A/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
166	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEE**Y**LKPLEEV
	E62Y/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
167	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	L72D/I92D	LN**D**AQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
168	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	L72H/I92D	LN**H**AQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
169	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV
	L72R/I92D	LN**R**AQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
170	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**D**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38D/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
171	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
172	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**Q**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38Q/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
173	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**A**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38A/I92D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
174	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/N88R	LNLAQSKNFHLRPRDLIS**R**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
175	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84R	LNLAQSKNFHLRPR**R**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
176	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84K	LNLAQSKNFHLRPR**K**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
177	hIL-2 F42A/Y45R/D20A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**A**KF**R**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
178	hIL-2 F42H/Y45R/D20A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**H**KF**R**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
179	hIL-2 R38D/E61R/D20A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**D**MLTFKFYMPKKATELKHLQCL**E**RELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
180	hIL-2 R38E/E61R/D20A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCL**E**RELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
181	hIL-2 R38Q/E61R/D20A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**Q**MLTFKFYMPKKATELKHLQCL**E**RELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
182	hIL-2 R38A/E61R/D20A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**A**MLTFKFYMPKKATELKHLQCL**E**RELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
183	hIL-2 R38A/D20A/E95A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**A**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
184	hIL-2 D20A/E95A/R38D	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**D**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
185	hIL-2 D20A/ E95A/R38E	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
186	hIL-2 D20A/E95A/R38Q	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**Q**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
187	hIL-2 D20A/E95A/F42R	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**R**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
188	hIL-2 D20A/E95A/F42A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**A**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
189	hIL-2 D20A/E95A/ F42D	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**D**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
190	hIL-2 D20A/E95A/ F42H	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**H**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
191	hIL-2 D20A/E95A/F42K	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**K**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
192	hIL-2 D20A/E95A/ K43A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTF**A**FYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
193	hIL-2 D20A/E95A/ K43E	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTF**E**FYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
194	hIL-2 D20A/E95A/ K43Q	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTF**Q**FYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
195	hIL-2 D20A/E95A/ Y45A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**A**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
196	hIL-2 D20A/E95A/ Y45K	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**K**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
197	hIL-2 D20A/E95A/ 45S	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKE**S**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
198	hIL-2 D20A/E95A/ Y45R	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**R**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
199	hIL-2 D20A/E95A/ E61A	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEAELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
200	hIL-2 D20A/E95A/ E62A	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEALKPLEEV LNLAQSKNFHLRPRDLISNINVIVLALKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
201	hIL-2 D20A/E95A/E62R	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEERLKPLEEV LNLAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
202	hIL-2 D20A/E95A/ E62K	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEKLKPLEEV LNLAQSKNFHLRPRDLISNINVIVLALKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
203	hIL-2 D20A/E95A/ E62Y	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEYLKPLEEV LNLAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
204	hIL-2 D20A/E95A/ E68Y	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEYV LNLAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
205	hIL-2 D20A/E95A/E68A	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEAV LNLAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
206	hIL-2 D20A/E95A/ E68L	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLELV LNLAQSKNFHLRPRDLISNINVIVLALKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
207	hIL-2 D20A/E95A/ L72Y	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNYAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
208	hIL-2 D20A/E95A/ L72R	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNRAQSKNFHLRPRDLISNINVIVLALKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
209	hIL-2 D20A/E95A/ L72A	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNAAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
210	hIL-2 D20A/E95A/L72D	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNDAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
211	hIL-2 D20A/E95A/ L72H	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNHAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
212	hIL-2 D20A/E95A/ L72F	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNFAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
213	hIL-2 F42K/Y45R/D20A/ S87A	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTKKFRMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLIANINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
214	hIL-2 F42K/Y45R/D20A/ E95A	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLTKKERMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLALKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
215	hIL-2 D20A/R38E/C125 A	APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT
216	hIL-2 T3A/D20A/R38E	APASSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
217	hIL-2 T3A/D20A/R38E/ C125A (IL-2-AAEA)	APASSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFAQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
218	hIL-2 Δ1-3APT/D20A/R38E	SSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEVLNL AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
219	hIL-2 Δ1-3APT/D20A/R38E/C125A	SSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEVLNL AQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITF**A**QSIISTLT
220	hIL-2 R38E/Q22A	APTSSSTKKTQLQLEHLLLDL**A**MILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
221	hIL-2 R38E/T123A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI**A**FCQSIISTLT
222	hIL-2 R38E/I129A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSI**A**STLT
223	hIL-2 R38E/S130A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSII**A**TLT
224	hIL-2 R38E/Q126A	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFC**A**SIISTLT
225	hIL-2 R38E/Q126D	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFC**D**SIISTLT
226	hIL-2 R38E/Q126V	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFC**V**SIISTLT
227	hIL-2 R38E/Q22A/S130A	APTSSSTKKTQLQLEHLLLDL**A**MILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSII**A**TLT
228	hIL-2 F42K/Y45R/Q126D	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**K**KF**R**MPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFC**D**SIISTLT
229	hIL-2 D20A/E95A/Q126D	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVL**A**LKGSETTFMCEYADETATIVEFLNRWITFC**D**SIISTLT
230	hIL-2 D20A/E61R	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**R**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
231	hIL-2 D20A/E61N	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**N**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
232	hIL-2 D20A/E61D	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**D**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
233	hIL-2 D20A/E61Q	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**Q**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
234	hIL-2 D20A/E61G	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**G**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
235	hIL-2 D20A/E61H	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**H**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
236	hIL-2 D20A/E61I	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**I**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
237	hIL-2 D20A/E61L	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**L**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
238	hIL-2 D20A/E61K	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**K**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
239	hIL-2 D20A/E61M	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**M**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
240	hIL-2 D20A/E61F	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**F**ELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
241	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**P**ELKPLEEV
	D20A/E61P	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
242	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**S**ELKPLEEV
	D20A/E61S	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
243	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**T**ELKPLEEV
	D20A/E61T	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
244	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**W**ELKPLEEV
	D20A/E61W	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
245	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**Y**ELKPLEEV
	D20A/E61Y	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
246	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLE**V**ELKPLEEV
	D20A/E61V	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
247	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**N**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42N	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
248	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**Q**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42Q	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
249	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**E**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42E	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
250	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**G**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42G	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
251	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**I**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42I	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
252	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**L**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42L	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
253	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**M**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42M	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
254	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**P**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42P	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
255	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**S**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42S	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
256	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**T**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42T	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
257	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**W**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42W	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
258	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**Y**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42Y	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
259	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLT**V**KFYMPKKATELKHLQCLEEELKPLEEV
	D20A/F42V	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
260	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**A**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45A	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
261	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**N**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45N	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
262	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**D**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45D	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
263	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**Q**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45Q	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
264	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**E**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45E	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
265	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**G**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45G	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
266	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**H**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45H	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
267	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**I**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45I	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
268	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**L**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45L	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
269	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**M**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45M	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
270	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**F**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45F	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
271	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**P**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45P	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
272	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**S**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45S	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
273	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**T**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45T	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
274	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**W**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45W	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
275	hIL-2	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLTRMLTFKF**V**MPKKATELKHLQCLEEELKPLEEV
	D20A/Y45V	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
276	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**N**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42N	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
277	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**Q**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42Q	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
278	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**E**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42E	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
279	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**G**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42G	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
280	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**I**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42I	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
281	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**L**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42L	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
282	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**K**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42K	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
283	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**M**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42M	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
284	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**P**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42P	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
285	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**S**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42S	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
286	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**T**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42T	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
287	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**W**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42W	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
288	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**Y**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42Y	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
289	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**V**KFYMPKKATELKHLQCLEEELKPLEEV
	I92D/F42V	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
290	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**A**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45A	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
291	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKE**N**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45N	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
292	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKE**D**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45D	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
293	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**Q**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45Q	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
294	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**E**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45E	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
295	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**G**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45G	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
296	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**H**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45H	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
297	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**I**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45I	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
298	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKE**L**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45L	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
299	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKE**M**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45M	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
300	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**F**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45F	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
301	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**P**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45P	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
302	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKF**S**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45S	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
303	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**T**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45T	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
304	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**W**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45W	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
305	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKF**V**MPKKATELKHLQCLEEELKPLEEV
	I92D/Y45V	LNLAQSKNFHLRPRDLISNINV**D**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
306	hIL-2	APTSSSTKKTQLQLEHLLL**H**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D20H	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
307	hIL-2	APTSSSTKKTQLQLEHLLL**S**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D20S	LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
308	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**A**KFYMPKKATELKHLQCLEEELKPLEEV
	F42A/N88R	LNLAQSKNFHLRPRDLIS**R**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
309	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**A**KFYMPKKATELKHLQCLEEELKPLEEV
	F42A/N88D	LNLAQSKNFHLRPRDLIS**D**INVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
310	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84A	LNLAQSKNFHLRPR**A**LISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
311	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84N	LNLAQSKNFHLRPR**N**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
312	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84Q	LNLAQSKNFHLRPR**Q**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
313	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84E	LNLAQSKNFHLRPR**E**LISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
314	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84G	LNLAQSKNFHLRPR**G**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
315	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84H	LNLAQSKNFHLRPR**H**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
316	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84I	LNLAQSKNFHLRPR**I**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
317	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84L	LNLAQSKNFHLRPR**L**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
318	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84M	LNLAQSKNFHLRPR**M**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
319	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84F	LNLAQSKNFHLRPR**F**LISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
320	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84P	LNLAQSKNFHLRPR**P**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
321	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84S	LNLAQSKNFHLRPR**S**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
322	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84T	LNLAQSKNFHLRPR**T**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
323	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84W	LNLAQSKNFHLRPR**W**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
324	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84Y	LNLAQSKNFHLRPR**Y**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
325	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/D84V	LNLAQSKNFHLRPR**V**LISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
326	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/I92A	LNLAQSKNFHLRPRDLISNINV**A**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
327	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/192R	LNLAQSKNFHLRPRDLISNINV**R**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
328	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/192N	LNLAQSKNFHLRPRDLISNINV**N**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
329	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/192Q	LNLAQSKNFHLRPRDLISNINV**Q**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
330	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/I92E	LNLAQSKNFHLRPRDLISNINV**E**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
331	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/I92G	LNLAQSKNFHLRPRDLISNINV**G**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
332	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/192H	LNLAQSKNFHLRPRDLISNINV**H**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
333	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/I92L	LNLAQSKNFHLRPRDLISNINV**L**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
334	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/I92K	LNLAQSKNFHLRPRDLISNINV**K**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
335	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/I92M	LNLAQSKNFHLRPRDLISNINV**M**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
336	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/I92F	LNLAQSKNFHLRPRDLISNINV**F**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
337	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/192P	LNLAQSKNFHLRPRDLISNINV**P**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
338	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/192S	LNLAQSKNFHLRPRDLISNINV**S**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
339	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/I92T	LNLAQSKNFHLRPRDLISNINV**T**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
340	hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV
	R38E/192W	LNLAQSKNFHLRPRDLISNINV**W**VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
341	hIL-2 R38E/192Y	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**Y**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
342	hIL-2 R38E/192V	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINV**V**VLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
343	hIL-2 R38E/H16E	APTSSSTKKTQLQL**E**ELLLDLQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
344	hIL-2 R38K/D20A	APTSSSTKKTQLQLEHLLL**A**LQMILNGINNYKNPKLT**K**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
345	WT hIL-2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
346	Human PD-1	PGWFLDSPDRPWNPPTESPALLVVTEGDNATFTCSESNTSESFVLNWYRMSPSNQTDKLAAFPEDRSQP GQDCRFRVTQLPNGRDFHMSVVRARRNDSGTYLCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSP SPRPAGQFQTLVVGVVGGLLGSLVLLVWVLAVICSRAARGTIGARRTGQPLKEDPSAVPVESVDYGELD FQWREKTPEPPVPCVPEQTEYATIVFPSGMGTSSPARRGSADGPRSAQPLRPEDGHCSWPL
347	Human PD-1	CCAGGATGGTTCTTAGACTCCCCAGACAGGCCCTGGAACCCCCCCACCTTCTCCCCAGCCCTGCTCGTG GTGACCGAAGGGGACAACGCCACCTTCACCTGCAGCTTCTCCAACACATCGGAGAGCTTCGTGCTAAAC TGGTACCGCATGAGCCCCAGCAACCAGACGGACAAGCTGGCCGCCTTCCCCGAGGACCGCAGCCAGCCC GGCCAGGACTGCCGCTTCCGTGTCACACAACTGCCCAACGGGCGTGACTTCCACATGAGCGTGGTCAGG GCCCGGCGCAATGACAGCGGCACCTACCTCTGTGGGGCCATCTCCCTGGCCCCCAAGGCGCAGATCAAA GAGAGCCTGCGGGCAGAGCTCAGGGTGACAGAGAGAAGGGCAGAAGTGCCCACAGCCCACCCCAGCCCC TCACCCAGGCCAGCCGGCCAGTTCCAAACCCTGGTGGTTGGTGTCGTGGGCGGCCTGCTGGGCAGCCTG GTGCTGCTAGTCTGGGTCCTGGCCGTCATCTGCTCCCGGGCCGCACGAGGGACAATAGGAGCCAGGCGC ACCGGCCAGCCCCTGAAGGAGGACCCCTCAGCCGTGCCTGTGTTCTCTGTGGACTATGGGGAGCTGGAT TTCCAGTGGCGAGAGAAGACCCCGGAGCCCCCCGTGCCCTGTGTCCCTGAGCAGACGGAGTATGCCACC ATTGTCTTTCCTAGCGGAATGGGCACCTCATCCCCCGCCCGCAGGGGCTCAGCTGACGGCCCTCGGAGT GCCCAGCCACTGAGGCCTGAGGATGGACACTGCTCTTGGCCCCTC
348	Anti-hPD-1 #1-mIgG2b-N297A HC	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRFT ISRDNSKNTLFLQMNSLRAEDTAVYYCATNDDYWGQGTLVTVSSAKTTPPSVYPLAPGCGDTTGSSVTL GCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVD KKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQ ISWFVNNVEVHTAQTQTHREDYASTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLV RAPQVYILPPPAEQLSRKDVSLTCLVVGENPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNM KTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
349	Anti-hPD-1 #1-mKappa LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARFSGSGSGT DFTLTISSLEPEDFAVYYCQQSSNWPRTFGQGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVCELNN FYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SENRNEC
350	Anti-hPD-1 #2-mIgG2b-N297A HC	QVQLVQSGVEVKKPGASVKVSCKASGYTFTNYYMYWVRQAPGQGLEWMGGINPSNGGTNENEKEKNRVT LTTDSSTTTAYMELKSLQFDDTAVYYCARRDYRFDMGFDYWGQGTTVTVSSAKTTPPSVYPLAPGCGDT TGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHP ASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVS EDDPDVQISWFVNNVEVHTAQTQTHREDYASTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTI SKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGENPGDISVEWTSNGHTEENYKDTAPVLDSDGSYF IYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
351	Anti-hPD-1 #2-mKappa LC	EIVLTQSPATLSLSPGERATLSCRASKGVSTSGYSYLHWYQQKPGQAPRLLIYLASYLESGVPARESGS GSGTDFTLTISSLEPEDFAVYYCQHSRDLPLTFGGGTKVEIKRADAAPTVSIFPPSSEQLTSGGASVVC FLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSENRNEC
352	IL-2RY	LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVENVEYMNCTWNSSSEPQPTNLTLHYWY KNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENL TLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKESLPSVDGQKRYTERVRSRENP LCGSAQHWSEWSHPIHWGSNTSKENPFLFALEAVVISVGSMGLIISLLCVYFWLERTMPRIPTLKNLED LVTEYHGNESAWSGVSKGLAESLQPDYSERLCLVSEIPPKGGALGEGPGASPCNQHSPYWAPPCYTLKP ET
353	human CD122 (IL-2Rβ)	AVNGTSQFTCFYNSRANISCVWSQDGALQDTSCQVHAWPDRRRWNQTCELLPVSQASWACNLILGAPDS QKLTTVDIVTLRVLCREGVRWRVMAIQDFKPFENLRLMAPISLQVVHVETHRCNISWEISQASHYFERH LEFEARTLSPGHTWEEAPLLTLKQKQEWICLETLTPDTQYEFQVRVKPLQGEFTTWSPWSQPLAFRTKP AALGKDTIPWLGHLLVGLSGAFGFIILVYLLINCRNTGPWLKKVLKCNTPDPSKFFSQLSSEHGGDVQK WLSSPFPSSSESPGGLAPEISPLEVLERDKVTQLLLQQDKVPEPASLSSNHSLTSCFTNQGYFFFHLPD ALEIEACQVYFTYDPYSEEDPDEGVAGAPTGSSPQPLQPLSGEDDAYCTFPSRDDLLLESPSLLGGPSP PSTAPGGSGAGEERMPPSLQERVPRDWDPQPLGPPTPGVPDLVDFQPPPELVLREAGEEVPDAGPREGV SFPWSRPPGQGEFRALNARLPLNTDAYLSLQELQGQDPTHLV

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
354	IL-2Rα	ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNT TKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRAL HRGPAESVCKMTHGKTRWTQPQLICTGEMETSQFPGEEKPQASPEGRPESETSCLVTTTDFQIQTEMAA TMETSIFTTEYQVAVAGCVELLISVLLLSGLTWQRRQRKSRRTI
355	L6 linker amino acid	SGGGGS
356	hIL-2-df-1H3-hkappa LC hIL-2 in italics	*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT*DTVLT QSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTDFTLTI DPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL*SSPVTKSENRGE C
357	hIL-2-L6-1H3-hKappa LC Linker in dashed underline hIL-2 in italics	*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLTS*GGGGG SDTVLTQSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGT DFTLTIDPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK SENRGEC
358	hIL-2-df-1H3-hIgG1 HC hIL-2 in italics	*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT*EVQLV ESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFTISRDN AKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDG VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK
359	hIL-2-L6-1H3-hIgG1 HC Linker in dashed underline hIL-2 in italics	*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKFYMPKKATELKHLQCLEEELKPLEEV* HRGPAESVCKMTHGKTRWTQPQLICT*SGGGGSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQM* HRGPAESVCKMTHGKTRWTQPQLICT*SGGGGSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQM* TISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKE NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
360	1H3-hIgG1-df-hIL-2 HC hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTESDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKL TRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMC EYADETATIVEFLNRWITFCQSIISTLT*
361	1H3-hIgG1-L6-hIL-2 HC Linker in dashed underline hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*SGGGGS*APTSSSTKKTQLQLEHLLLDLQMILNGINN *YKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGS ETTEMCEYADETATIVEFLNRWITFCQSIISTLT*
362	1H3-hKappa-df-hIL-2 (WT) LC hIL-2 in italics	DTVLTQSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTD FTLTIDPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKFYMPKKATELKHLQCLEEEL KPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTL T*

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
363	1H3-hKappa-L6-hIL-2 (WT) LC	DTVLTQSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTD FTLTIDPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC*SGGGGS**APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQ*
	underline hIL-2 in italics	*CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITECQ SIISTLT*
364	L20 linker	SGGGGSGGGGSGGGGSGGGS
365	hCD25-L20-hIL-2-df-1H3-hIgG1 HC	ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNT TKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRAL HRGPAESVCKMTHGKTRWTQPQLICT*SGGGGSGGGGSGGGGSGGGS**APTSSSTKKTQLQLEHLLLDLQM*
	Linker in dashed underline hIL-2 in italics	*ILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVI VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT*EVQLVESGGGLVQPGRSLKLSCAVSGFT FSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFTISRDNAKITLYLQMDSLRSEDTATYYCA RHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK
366	hCD25-L20-hIL-2-L6-1H3-hIgG1 HC	ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNT TKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRAL HRGPAESVCKMTHGKTRWTQPQLICT*SGGGGSGGGGSGGGGSGGGS**APTSSSTKKTQLQLEHLLLDLQM*
	Linkers in dashed	*ILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVI VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT**SGGGGS*EVQLVESGGGLVQPGRSLKLSC
	underline hIL-2 in italics	AVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFTISRDNAKITLYLQMDSLRSEDT ATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK
367	hCD25-L20-hIL-2-df-1H3-hKappa LC	ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGERRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNT TKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRAL HRGPAESVCKMTHGKTRWTQPQLICT*SGGGGSGGGGSGGGGSGGGS**APTSSSTKKTQLQLEHLLLDLQM*
	Linker in dashed underline hIL-2 in italics	*ILNGINNYKNPKLTRMLTEKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVI VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT*DTVLTQSPALAVSPGERVTISCRASESV RTGVHWYQQKPGQQPKLLIYGASNLESGVPARESGSGSGTDFTLTIDPVEADDTATYFCQQSWNDPFTE GSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSENRGEC
368	hCD25-L20-hIL-2-L6-1H3-hKappa LC	ELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNT TKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRAL HRGPAESVCKMTHGKTRWTQPQLICT*SGGGGSGGGGSGGGGSGGGS**APTSSSTKKTQLQLEHLLLDLQM*
	Linkers in dashed	*ILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVI VLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT**SGGGGS*DTVLTQSPALAVSPGERVTISC
	underline hIL-2 in italics	RASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTDFTLTIDPVEADDTATYFCQQSW NDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSENRGEC
369	1H3-hIgG1-df - hCD25-L20-hIL-2 HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
	Linker in dashed underline hIL-2 in italics	NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGERR IKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCR EPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICT*SGGGGSGGGG*
		*SGGGGSGGGS**APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKFYMPKKATELKHLQCL*
		EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSI ISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
370	1H3-hIgG1-L6-hCD25-L20-hIL-2 HC Linkers in dashed underline hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWI TFCQSIISTLT
371	1H3-hKappa-df-hCD25-L20-hIL-2 LC Linker in dashed underline hIL-2 in italics	DTVLTQSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTD FTLTIDPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGECELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGERRIKSGSLYMLCTGNSSHSSWDNQCQCTS SATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQMVYYQCV QGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGGGSGGGGSGGGGSGGGGSAPTSSSTKKTQLQLEHL LLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLI SNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
372	1H3-hKappa-L6-hCD25-L20-hIL-2 LC Linkers in dashed underline hIL-2 in italics	DTVLTQSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTD FTLTIDPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGECSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCECKRGERRIKSGSLYMLCTGNSSHSSWDN QCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQASLPGHCREPPPWENEATERIYHFVVGQM VYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGGGSGGGGSGGGGSGGGGSAPTSSSTKKTQ LQLEHLLLDLQMILNGINNYKNPKLTRMLTEKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNEHL RPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
373	H7-02-hIgG4 HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFKSYAMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWINGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
374	1H3-hkappa LC	DTVLTQSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTD FTLTIDPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC
375	2D12-mIgG1-D265A-L6-hIL-2 HC	EVQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGINPNNGGTTYNQKFKGKAT LTVDKSSSTAYMELRSLTSQDSAVYYCARDYYRYGHYYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGSA AQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVA HPASSTKVDKKIVPRDCGCKPCICTVPEVSSVFIFPPKPKDVLTITLTPKVTCVVVAISKDDPEVQESW FVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAP QVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKS NWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGKSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNY KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFCQSIISTLT
376	2D12-mkappa LC	QIVLTQSPAIMSASPGEKVTMTCSVSSSVREMHWYQQKSGTSPKRWIYDTSKLASGVPARFSGSGSGTS YSLTISSMEAEDAATYYCQQWSSNPPTFGGGTKLKIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNF YPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS FNRNEC
377	hIL-2 Q126L	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCLSIISTLT
378	hIL-2 Q126E	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCESIISTLT
379	1H3-hIgG1 HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
		WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
380	huPD-1-Fc	MQIPQAPWPVVWAVLQLGWRPGWELDSPDRPWNPPTESPALLVVTEGDNATFTCSESNTSESFVLNWYR MSPSNQTDKLAAFPEDRSQPGQDCRFRVTQLPNGRDFHMSVVRARRNDSGTYLCGAISLAPKAQIKESL RAELRVTERRAEVPTAHPSPSPRPAGQFQTEGRMDPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
381	cynomolgous-PD-1-Fc	MQIPQAPWPVVWAVLQLGWRPGWFLESPDRPWNAPTFSPALLLVTEGDNATFTCSFSNASESFVLNWYR MSPSNQTDKLAAFPEDRSQPGQDCRERVTRLPNGRDFHMSVVRARRNDSGTYLCGAISLAPKAQIKESL RAELRVTERRAEVPTAHPSPSPRPAGQFQIEGRMDPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
382	2H7 VH	GAGGTGCAGCTGCTGGAAAGCGGCGGCGGACTGGTGCAGCCTGGAGGCAGCCTGCGGCTGTCTTGTGCC GCTTCTGGCTTCACCTTCAAGGACTACTGCATGACCTGGGTCAGACAGGCCCCTGGCAAGGGCCTCGAG TGGGTGTCCGCCATCGTGTACAGCGGCGGGTCAACATACTACGCCGACAGCGTGAAGGGCAGATTCACA ATCAGCAGAGATAACAGCAAGAACACCCTGTACCTGCAGATGAACAACCTGAGAGCTGAAGATACCGCC GTGTACTACTGCGCCAAGTACACCAGAGCCAGCTACTTCTACGACGCCATGGACGTGTGGGGCCAGGGC ACCACCGTGACAGTGTCCTCAT
383	2H7 VL	GAGATCGTGCTGACCCAGTCTCCTGGCACCCTGAGCCTGAGCCCTGGCGAGAGAGCTACACTGTCATGC AGAGCCTCTCAGAGCATCGGCAAGAGCTTCCTGGCCTGGTACCAGCAAAAGCCTGGACAGGCCCCTAGA CTGCTGATCTACGACGCCAGCACCAGAGCCGCTGATATCCCCGCCAGATTCAGCGGATCTGGCAGCGGC ACTGATTTCACCCTCACCATCAGCAGCCTGGAACCCGAGGACTTCGCCGTGTACTACTGCCAGCAGTAC TACGACTGGCCCCCCCTGTCTTTTGGCGGAGGCACAAAGGTGGAAATCAAG
384	2H7 VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSS
385	2H7 VL	EIVLTQSPGTLSLSPGERATLSCRASQSIGKSFLAWYQQKPGQAPRLLIYDASTRAADIPARFSGSGSG TDFTLTISSLEPEDFAVYYCQQYYDWPPLSFGGGTKVEIK
386	2H7 HCDR1	GFTFKDYCMT
387	2H7 HCDR2	AIVYSGGSTYYADSVKG
388	2H7 HCDR3	YTRASYFYDAMDV
389	2H7 LCDR1	RASQSIGKSFLA
390	2H7 LCDR2	DASTRAA
391	2H7 LCDR3	QQYYDWPPLS
392	C51E6-5 VH	CAGGTTCAGCTGGTTCAGTCTGGCAGCGAGCTGAAGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAG GCCTCTGGCTACAGCCTGTACGGCACCTCTATGCACTGGGTCCGACAGGCTCCAGGACAGGGACTTGAG TGGATGGGCTACATCAGCCCCTTTACCGGCAGAGCCACATACGCCCAGGGCTTCACAGGCAGATTCGTG TTCAGCCTGGACACCAGCGTGTCCACAGCCTACCTGCAGATCAGCTCTCTGAAGGCCGAGGACACCGCC GTGTACTACTGCGCCAGAGACTACGACTACCGGTACTACTATGCCATGGACTACTGGGGCCAGGGCACC ACAGTTACAGTGTCCTCA
393	C51E6-5 VL	GAAATTGTGCTGACACAGAGCCCCGACTTCCAGAGCGTGACCCCTAAAGAAAAAGTGACCATCACCTGT ACCGCCAGCGAGTCCGTGCCTCCTCAGTTCCTGCATTGGTATCAGCAGAAGCCCGATCAGAGCCCCAAG CTGCTGATCTACGCCAGCAGAGAAAGAGCCAGCGGCGTCCCAAGCAGATTTTCTGGCTCTGGCAGCGGC ACCGACTTCACCCTGACAATCAATAGCCTGGAAGCCGAGGACGCCGCCACCTACTACTGCCACCAGTTT CACAGAAGCCCTCTGACCTTTGGCGGAGGCACCAAGCTGGAAATCAAG
394	C51E6-5 VH	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSS
395	C51E6-5 VL	EIVLTQSPDFQSVTPKEKVTITCTASESVPPQFLHWYQQKPDQSPKLLIYASRERASGVPSRESGSGSG TDFTLTINSLEAEDAATYYCHQFHRSPLTFGGGTKLEIK
396	C51E6-5 HCDR1	GYSLYGTSMH
397	C51E6-5 HCDR2	YISPFTGRATYAQGFTG
398	C51E6-5 HCDR3	DYDYRYYYAMDY
399	C51E6-5 LCDR1	TASESVPPQFLH

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
400	C51E6-5 LCDR2	ASRERAS
401	C51E6-5 LCDR3	HQFHRSPLT
402	A2 VH	GACGTGCAGCTGGTGGAAAGCGGCGGAGGCCTGGTCCAGCCCGGCGGCTCTCTGAGACTGAGCTGCGCC GCCAGCGGCTTCACCTTCGACATCAGCGCCATGAGCTGGGTGCGGCAGGCCCCTGGCAAGGGCCTGGAA TGGGTCAGCACAATCAGCGGATCTGCCTACAGCACCTACTACGCCGACAGCGTGAAGGGCAGATTCACC ATCTCAAGAGATAACAGCAAGAGCACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCC GTGTACTACTGCGCCAGAGAGATCTTCAGCGACTACTGGGGCTTGGGCACCCTGGTGACAGTGTCCTCA
403	A2 VL	CAAAGCGTGCTGACACAGCCCCCCAGCGCTTCTGGCACCCCTGGCCAGAGAGTGACCATCTCATGCAGC GGGTCAACAAGCAACATCGGCAGAGAGAGCGTGTACTGGTACCAGCAGCTGCCTGGAACCGCCCCTAAG CTGCTGATCTACAGCAACGTGCAGCGGCCTAGCGGCGCCCCTAACAGATTCAGCGGCAGCAAGAGCGGC ACCAGCGCCAGCCTGGCCATCAGCGGCCTGCAGAGCGAGGACGAGGCCGACTACTACTGCGGCACATGG GACGACAGCCTGAACGGCTGGGTGTTCGGCGGCGGAACTAAGCTGACCGTCCTA
404	A2 VH	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSS
405	A2 VL (OMC479p1.A2VL)	QSVLTQPPSASGTPGQRVTISCSGSTSNIGRESVYWYQQLPGTAPKLLIYSNVQRPSGAPNRESGSKSG TSASLAISGLQSEDEADYYCGTWDDSLNGWVFGGGTKLTVL
406	A2 HCDR1	GFTFDISAMS
407	A2 HCDR2	TISGSAYSTYYADSVKG
408	A2 HCDR3	EIFSDY
409	A2 LCDR1	SGSTSNIGRESVY
410	A2 LCDR2	SNVQRPS
411	A2 LCDR3	GTWDDSLNGWV
412	H7-767 HC	GAGGTGCAGCTGCTGGAAAGCGGCGGCGGCCTCGTGCAGCCTGGCGGATCTCTGCGGCTGAGCTGTGCT GCCAGCGGCTTCACATTTAAATCCTACGCCATGCACTGGGTTAGACAAGCCCCCGGAAAGGGCCTGGAA TGGGTGTCCGCCATCGTCTACAGCGGCGGATCTACATACTACGCCGACAGCGTGAAGGGCCGGTTCACC ATCAGCAGAGATAATAGCAAGAACACCCTGTACCTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCC GTGTACTACTGCGCCAAGTACGACAGAGCTTCTTATTTCTACGATGCCATGGACGTGTGGGGCCAGGGC ACCACCGTGACAGTGTCCTCAGCTAGCACCAAGGGCCCTAGCGTGTTTCCACTGGCCCCTAGCTCTAAA AGCACAAGCGGCGGAACCGCCGCTCTGGGTTGTCTGGTGAAGGACTACTTCCCTGAGCCTGTGACCGTC AGCTGGAACAGCGGCGCCCTGACCAGCGGCGTTCACACATTCCCCGCTGTGCTGCAGAGCTCTGGGCTG TACAGCCTGAGCAGCGTGGTGACCGTGCCTTCTTCTTCTCTGGGCACACAAACATACATCTGCAACGTG AACCACAAGCCCAGTAATACCAAAGTGGATAAGAAGGTGGAACCTAAGTCTTGCGACAAGACCCACACC TGTCCTCCGTGCCCTGCTCCTGAACTGgctGGAgctCCCAGCGTGTTCCTGTTCCCCCCCAAACCTAAA GACACCCTGATGATCAGCCGGACCCCTGAGGTGACCTGCGTGGTCGTCGACGTGTCCCACGAAGATCCT GAGGTGAAGTTCAACTGGTACGTGGACGGCGTGGAAGTGCATAATGCCAAGACAAAGCCTAGAGAGGAA CAGTACAACAGCACCTATAGAGTGGTGTCCGTGCTGACAGTGCTGCACCAGGACTGGCTGAACGGCAAG GAATACAAGTGCAAGGTGTCCAACAAGGCCCTCCCCGCCCCTATCGAGAAGACCATCAGCAAGGCAAAG GGCCAACCTAGAGAGCCCCAGGTGTACACCCTGCCTCCAAGCAGAGATGAGCTGACCAAGAACCAGGTT AGCCTGACTTGTCTGGTGAAAGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCAACGGCCAG CCTGAGAACAACTACAAGACCACACCTCCAGTGCTGGACAGCGACGGCAGCTTCTTCCTGTATAGCAAG CTGACAGTGGACAAGAGCAGATGGCAGCAGGGCAACGTGTTCAGCTGCAGCGTCATGCACGAGGCCCTG CACAACCACTACACCCAGAAGTCTCTGAGCCTGAGCCCTGGAAAGGCCCCTGCTTCTAGCAGCACCAAG AAGACCCAGCTGCAGCTGGAACACCTGCTGCTGGCCCTGCAGATGATCCTGAACGGCATCAACAACTAC AAGAACCCCAAGCTGACCGAGATGCTGACATTTAAGTTCTACATGCCTAAGAAAGCCACCGAGCTGAAG CACCTGCAATGTCTGGAAGAAGAGCTGAAACCTCTGGAAGAGGTGCTGAATCTGGCTCAGTCAAAGAAC TTCCACCTTAGACCTAGAGATCTGATCAGCAACATCAACGTGATCGTGCTGGAACTGAAGGGCAGCGAG ACGACCTTCATGTGCGAGTACGCCGACGAGACAGCCACAATCGTGGAGTTCCTGAACAGATGGATCACC TTCGCCCAGAGCATCATCTCCACCCTGACC
413	H7-767 LC	GAGATCGTGCTGACCCAGTCCCCAGGCACACTGAGCCTGAGCCCCGGCGAGCGGGCCACCCTGAGCTGT AGAGCTAGCCAGAGCATCTCCAGCAGCTTCCTGGCCTGGTACCAGCAGAAACCTGGCCAGGCCCCTAGA CTGCTGATCTACGACGCCTCTGATAGAGCTACAGGCATCCCCGACCGGTTCAGCGGCAGCGGATCTGGC ACCGACTTCACCCTGACCATCAGCAGACTCGAGCCTGAAGATTTCGCCGTGTACTACTGCCAGCAATAC TATGACTGGCCTCCTCTGTCTTTTGGCGGCGGAACAAAGGTGGAAATTAAGCGTACGGTGGCGGCGCCC AGCGTGTTCATCTTCCCACCCAGCGACGAGCAGCTGAAGTCCGGCACAGCCAGCGTGGTGTGCCTGCTG AACAACTTCTACCCCCGCGAGGCCAAGGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAGC CAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGC AAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCCAGCCCCGTG ACCAAGAGCTTCAACCGGGGCGAGTGC

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
414	H7-632 HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFKSYAMHWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT
	CDRs solid	ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYDRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK
	underlined	STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
	Constant	NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP
	region dashed	EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
	underlined	GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
		LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
415	H7-632 LC	EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQKPGQAPRLLIYDASDRATGIPDRESGSGSG
	CDRs solid	TDFTLTISRLEPEDFAVYYCQQYYDWPPLSFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL
	underlined	NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPV
	Constant	KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGS*APTSSSTKKTQLQLEHLLLALQMILNGIN*
	region dashed underlined	
416	H7-632 VH	EVQLLESGGGLVQPGGSLRLSCAASGFTFKSYAMHWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET
		ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYDRASYFYDAMDVWGQGTTVTVSS
417	H7-632 VL	EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQKPGQAPRLLIYDASDRATGIPDRESGSGSG
		TDFTLTISRLEPEDFAVYYCQQYYDWPPLSFGGGTKVEIK
418	H7-632 HCDR1	GFTFKSYAMH
419	H7-632 HCDR2	AIVYSGGSTYYADSVKG
420	H7-632 HCDR3	YDRASYFYDAMDV
421	H7-632 LCDR1	RASQSISSSFLA
422	H7-632 LCDR2	DASDRAT
423	H7-632 LCDR3	QQYYDWPPLS
424	2H7-hIgG4 HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVEPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
425	2H7-hkappa LC	EIVLTQSPGTLSLSPGERATLSCRASQSIGKSFLAWYQQKPGQAPRLLIYDASTRAADIPARESGSGSG TDFTLTISSLEPEDFAVYYCQQYYDWPPLSFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPV TKSENRGEC
426	C51E6-5-hIgG4 HC	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGREV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVEPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
427	C51E6-5-hKappa LC	EIVLTQSPDFQSVTPKEKVTITCTASESVPPQFLHWYQQKPDQSPKLLIYASRERASGVPSRESGSGSG TDFTLTINSLEAEDAATYYCHQFHRSPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT KSENRGEC
428	A2-hIgG4 HC	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLG

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
429	A2-hLambda LC	QSVLTQPPSASGTPGQRVTISCSGSTSNIGRESVYWYQQLPGTAPKLLIYSNVQRPSGAPNRESGSKSG TSASLAISGLQSEDEADYYCGTWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLEPPSSEELQANKATLVC LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE KTVAPTECS
430	2H7-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGKA*PTSSSTKKTQLQLEHLLLALQMILNGINNYKNP* *KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTE* *MCEYADETATIVEFLNRWITFCQSIISTLT*
431	H7-632-hIgG1-LAGA-df-hIL-2 (T3A/C125A) HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFKSYAMHWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYDRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTIMISRTPEVTCVVVDVSHEDP EVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPASSSTKKTQLQLEHLLLDLQMIINGINNY KNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVINLAQSKNFHERPRDLISNINVIVLELKGSE ITEMCEYADETATIVEFLNRWITFAQSIISTLT
432	C51E6-5-hIgG4-L6-hIL-2 (D20A/R38E) HC Linker in dashed underline hIL-2 in italics	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGS*APTSSSTKKTQLQLEHLLLALQMILNGIN* -------- *NYKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKG* *SETTEMCEYADETATIVEFLNRWITFCQSIISTLT*
433	A2-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGKA*PTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLT* *FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADE* *TATIVEFLNRWITFCQSIISTLT*
434	1H3-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKA*PTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEM* *LTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYA* *DETATIVEFLNRWITFCQSIISTLT*
435	2H7-hIgG4-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVEPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGKA*PASSSTKKTQLQLEHLLLALQMILNGINNYKNP* *KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTE* *MCEYADETATIVEFLNRWITFAQSIISTLT*
436	hPD-1 extracellular domain	CCAGGATGGTTCTTAGACTCCCCAGACAGGCCCTGGAACCCCCCCACCTTCTCCCCAGCCCTGCTCGTG GTGACCGAAGGGGACAACGCCACCTTCACCTGCAGCTTCTCCAACACATCGGAGAGCTTCGTGCTAAAC TGGTACCGCATGAGCCCCAGCAACCAGACGGACAAGCTGGCCGCCTTCCCCGAGGACCGCAGCCAGCCC GGCCAGGACTGCCGCTTCCGTGTCACACAACTGCCCAACGGGCGTGACTTCCACATGAGCGTGGTCAGG GCCCGGCGCAATGACAGCGGCACCTACCTCTGTGGGGCCATCTCCCTGGCCCCCAAGGCGCAGATCAAA GAGAGCCTGCGGGCAGAGCTCAGGGTGACAGAGAGAAGGGCAGAAGTGCCCACAGCCCACCCCAGCCCC TCACCCAGGCCAGCCGGCCAGTTCCAA

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
437	hPD-1 extracellular domain HC	PGWFLDSPDRPWNPPTFSPALLVVTEGDNATFTCSFSNTSESFVLNWYRMSPSNQTDKLAAFPEDRSQP GQDCRFRVTQLPNGRDFHMSVVRARRNDSGTYLCGAISLAPKAQIKESLRAELRVTERRAEVPTAHPSP SPRPAGQFQ
438	OMC. 1. B6-hIgG4 HC	EVQLLESGGGLVQPGGSLRLSCAASGFTESSNYMSWVRQAPGKGLEWVSAISSSGGTIFYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCAKHKWNAVYYDGMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
439	OMC.1. B6-hLambda LC	QSVLTQPPSASGTPGQRVTISCSGSNSNIGRNLVNWYQQLPGTAPKLLIYTIDQRPSGVPDRESGSKSG TSASLVISGLQSEDEADYYCAAWDGSLNAWVFGGGTKLTVLGQPKAAPSVTLEPPSSEELQANKATLVC LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE KTVAPTECS
440	OMC.2. C6-hIgG4 HC	EVQLLESGGGLVQPGGSLRLSCTASGFTESSYEMQWVRQAPGKGLEWVLGITSSSSHIFYADSVKGRET VSRDNSKNTLYLQMNSLRAEDTAVYYCTKDLNSYYGLDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENW YVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREP QVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKS RWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
441	OMC.2.C6-hLambda LC	QSVMTQPPSASGTPGQRVTISCSGSTSNLGNNYVSWYQHLPGTAPKLLIYGNDQRPSGVPDRESGSKSG TSASLAISGLQSDDEADYYCSSWDASLNVWVFGGGTKLTVLGQPKAAPSVTLEPPSSEELQANKATLVC LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE KTVAPTECS
442	OMC. 1. D6-hIgG4 HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYYMSWVRQAPGKGLEWVSAISSSGGTIFYADSVKGRFI ISRDNSKNTLYLQMNSLRAEDTAVYYCAKHKWNDVYYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
443	OMC.1.D6-hLambda LC	QSVLTQPPSASGTPGQRVTISCSGSNSNIGRNLVNWYQQLPGTAPKLLIYTVDQRPSGVPDRESGSKSG TSASLAISGLASEDEADYYCAAWDSSLNSWVFGGGTKLTVLGQPKAAPSVTLEPPSSEELQANKATLVC LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE KTVAPTECS
444	D12-hIgG4 HC	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRET ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTAA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLG
445	D12-hLambda LC	QSVLTQPPSASGTPGQRVTISCSGNTSNIGRESVYWYQQLPGTAPKLLIYSNVQRPSGVPDRESGSKSG TSASLAISGLQSEDEADYYCGTWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLEPPSSEELQANKATLVC LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE KTVAPTECS
446	G12-hIgG4 HC	DSLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFTI SRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTK VDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMHEALHNHYTQKSLSLSLG
447	G12-hLambda LC	QSVLTQPPSASGTPGQRVTISCSGSTSNIGRESVYWYQQLPGTAPKLLIYLNSQRPSGVPDRESGSKSG TSASLAISGLQSEDVADYYCGTWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLEPPSSEELQANKATLVC LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE KTVAPTECS
448	pCMV6-hygro-HA-cyno-PD-1 (1-185)	aacaaaatattaacgcttacaatttccattcgccattcaggctgcgcaactgttgggaagggcgatcgg tgcgggcctcttcgctattacgccagctggcgaaaggggatgtgctgcaaggcgattaagttgggtaa cgccagggttttcccagtcacgacgttgtaaaacgacggccagtgccaagctgatctatacattgaatc aatattggcaattagccatattagtcattggttatatagcataaatcaatattggctattggccattgc atacgttgtatctatatcataatatgtacatttatattggctcatgtccaatatgaccgccatgttgac attgattattgactagttattaatagtaatcaattacggggtcattagttcatagcccatatatggagt

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
		tccgcgttacataacttacggtaaatggcccgcctggctgaccgcccaacgacccccgcccattgacgt
		caataatgacgtatgttcccatagtaacgccaatagggactttccattgacgtcaatgggtggagtatt
		tacggtaaactgcccacttggcagtacatcaagtgtatcatatgccaagtccgcccccattgacgtca
		atgacggtaaatggcccgcctggcattatgcccagtacatgaccttacgggacttttcctacttggcagt
		acatctacgtattagtcatcgctattaccatggtgatgcggttttggcagtacaccaatgggcgtggat
		agcggtttgactcacggggatttccaagtctccaccccattgacgtcaatgggagtttgttttggcacc
		aaaatcaacgggactttccaaaatgtcgtaataaccccgccccgttgacgcaaatgggcggtaggcgtg
		tacggtgggaggtctatataagcagagctcgtttagtgaaccgtcagaattttgtaatacgactcacta
		tagggcggccgggaattcgtcgactggatccggtaccgaggagatctgccgccgcgatcgccggcgcgc
		cagatctcaagcttatggacatgcgggtgccagcacaacttctcggattactattgttatggctgcgag
		gtgcgcgctgttatccttacgacgtgcctgactacgccccaggatggttcttagagtccccagacaggc
		cctggaacgccccacctttctccccagccctgctcctggtgaccgaaggggacaacgccacccttcacct
		gcagcttctccaacgcatcggagagcttcgtgctaaactggtacaggatgagccccagcaaccagacgg
		acaagctggccgccttccccgaggaccgcagccagcccggccaggactgccgcttccgtgtcacacgcc
		tgcccaacgggcgtgacttccacatgagcgtggtcagggcccggcgcaatgacagcggcacctacctct
		gtggggccatctccctggcccccaaggcgcagatcaaagagagcctgcgggcagagctcagggtgacag
		agagaagggcagaagtgcccacagcccaccccagccctcacccaggccagccggccagttccaagccc
		tggtggttggtgtcgtgggcggcctgctgggcagcctggtgctgctagtctgggtcctggccgtcatct
		gctcccgcgccgcacaagggacaatagaagccaggcgcacctgacgcgttaagcggccgcactcgaggt
		ttaaacggccggccgcggtcatagctgtttcctgaacagatcccgggtggcatccctgtgacccctccc
		cagtgcctctcctggccctggaagttgccactccagtgcccaccagccttgtcctaataaaattaagtt
		gcatcattttgtctgactaggtgtccttctataatattatggggtggaggggggtggtatggagcaagg
		ggcaagttgggaagacaacctgtagggcctgcggggtctattgggaaccaagctggagtgcagtggcac
		aatcttggctcactgcaatctccgcctcctgggttcaagcgattctcctgcctcagcctcccgagttgt
		tgggattccaggcatgcatgaccaggctcagctaatttttgtttttttggtagagacggggtttcacca
		tattggccaggctggtctccaactcctaatctcaggtgatctacccaccttggcctcccaaattgctgg
		gattacaggcgtgaaccactgctcccttccctgtccttctgattttaaaataactataccagcaggagg
		acgtccagacacagcataggctacctggccatgcccaaccggtgggacatttgagttgcttgcttggca
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		gttccgcccattctccgcccccatggctgactaatttttttttatttatgcagaggccgaggccgcctcgg
		cctctgagctattccagaagtagtgaggaggctttttggaggcctaggcttttgcaaaaagctcccgg
		gagcttgtatatccattttcggatctgatcaagagacacgtacgaccatgaaaaagcctgaactcaccg
		cgacgtctgttgagaagtttctgatcgaaaagttcgacagcgtctccgacctgatgcagctctcggagg
		gcgaagaatctcgtgctttcagcttcgatgtaggagggcgtggatatgtcctgcgggtaaatagctgcg
		ccgatggtttctacaaagatcgttatgtttatcggcactttgcatcggccgcgctcccgattccggaag
		tgcttgacattggggaatttagcgagagcctgacctattgcatctcccgccgtgcacagggtgtcacgt
		tgcaagacctgcctgaaaccgaactgcccgctgttctgcaaccggtcgcggaggccatggatgcaatcg
		ctgcggccgatcttagccagacgagcgggttcggcccattcggaccgcaaggaatcggtcaatacacta
		catggcgtgatttcatatgcgcgattgctgatccccatgtgtatcactggcaaactgtgatggacgaca
		ccgtcagtgcgtccgtcgcgcaggctctcgatgagctgatgctttgggccgaggactgccccgaagtcc
		ggcacctcgtgcacgcggatttcggctccaacaatgtcctgacggacaatggccgcataacagcggtca
		ttgactggagcgaggcgatgttcggggattcccaatacgaggtcgccaacatcttcttctggaggccgt
		ggttggcttgtatggagcagcagacgcgctacttcgagcggaggcatccggagcttgcaggatcgccgc
		ggctccgggcgtatatgctccgcattggtcttgaccaactctatcagagcttggttgacggcaatttcg
		atgatgcagcttgggcgcagggtcgatgcgacgcaatcgtccgatccggagccgggactgtcgggcgta
		cacaaatcgcccgcagaagcgcggccgtctggaccgatggctgtgtagaagtactcgccgatagtggaa
		accgacgccccagcactcgtccgagggcaaaggaatagctgcagcgggactctggggttcgaaatgacc
		gaccaagcgacgcccaacctgccatcacgagatttcgattccaccgccgccttctatgaaaggttgggc
		ttcggaatcgttttccgggacgccggctggatgatcctccagcgcggggatctcatgctggagttcttc
		gcccaccccaacttgtttattgcagcttataatggttacaaataaagcaatagcatcacaaatttcaca
		aataaagcatttttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatcatgtc
		tgtataccgtcgacctctagctagagcttggcgtaatcatggtcatagctgtttcctgtgtgaaattgtt
		tatccgctcacaattccacacaacatacgagccggaagcataaagtgtaaagcctggggtgcctaatga
		gtgagctaactcacattaattgcgttgcgctcactgcccgctttccagtcgggaaacctgtcgtgccag
		ctgcattaatgaatcggccaacgcgcggggagaggcggtttgcgtattgggcgctcttccgcttcctcg
		ctcactgactcgctgcgctcggtcgttcggctgcggcgagcggtatcagctcactcaaaggcggtaata
		cggttatccacagaatcaggggataacgcaggaaagaacatgtgagcaaaaggccagcaaaaggccagg
		aaccgtaaaaaggccgcgttgctggcgtttttccataggctccgccccctgacgagcatcacaaaaat
		cgacgctcaagtcagaggtggcgaaacccgacaggactataaagataccaggcgtttcccccctggaagc
		tccctcgtgcgctctcctgttccgaccctgccgcttaccggatacctgtccgcctttctcccttcgggaa
		agcgtggcgctttctcatagctcacgctgtaggtatctcagttcggtgtaggtcgttcgctccaagctg
		ggctgtgtgcacgaacccccgttcagcccgaccgctgcgccttatccggtaactatcgtcttgagtcc
		aacccggtaagacacgacttatcgccactggcagcagccactggtaacaggattagcagagcgaggtat
		gtaggcggtgctacagagttcttgaagtggtggcctaactacggctacactagaagaacagtatttggt
		atctgcgctctgctgaagccagttaccttcggaaaaagagttggtagctcttgatccggcaaacaaacc
		accgctggtagcggtggtttttttgtttgcaagcagcagattacgcgcagaaaaaaaggatctcaagaa
		gatcctttgatcttttctacggggtctgacgctcagtggaacgaaaactcacgttaagggatttttggtc
		atgagattatcaaaaaggatcttcacctagatccttttaaattaaaaatgaagttttaaatcaatctaa
		agtatatatgagtaaacttggtctgacagttaccaatgcttaatcagtgaggcacctatctcagcgatc
		tgtctatttcgttcatccatagttgcctgactccccgtcgtgtagataactacgatacgggagggctta
		ccatctggccccagtgctgcaatgataccgcgagacccacgctcaccggctccagatttatcagcaata
		aaccagccagccggaagggccgagcgcagaagtggtcctgcaactttatccgcctccatccagtctatt

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
		aattgttgccgggaagctagagtaagtagttcgccagttaatagtttgcgcaacgttgttgccattgct acaggcatcgtggtgtcacgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaagg cgagttacatgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttactgtcatgcca tccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctgagaatagtgtatgcggcga ccgagttgctcttgcccggcgtcaatacgggataataccgcgccacatagcagaactttaaaagtgctc atcattggaaaacgttcttcggggcgaaaactctcaaggatcttaccgctgttgagatccagttcgatg taacccactcgtgcacccaactgatcttcagcatcttttactttcaccagcgtttctgggtgagcaaaa acaggaaggcaaaatgccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttc cttttcaatattattgaagcatttatcagggttattgtctcatgagcggatacatatttgaatgtatt tagaaaaataaacaaatagggggttccgcgcacatttccccgaaaagtgccacctgacgcgccctgtagc ggcgcattaagcgcggcgggtgtggtggttacgcgcagcgtgaccgctacacttgccagcgccctagcg cccgctcctttcgctttcttcccttcctttctcgccacgttcgccggctttccccgtcaagctctaaat cgggggctcccttttagggttccgatttagtgctttacggcacctcgaccccaaaaaacttgattagggt gatggttcacgtagtgggccatcgccctgatagacggtttttcgccctttgacgttggagtccacgttc tttaatagtggactcttgttccaaactggaacaacactcaaccctatctcggtctattcttttgattta taagggattttgccgatttcggcctattggttaaaaaatgagctgatttaacaaaaatttaacgcgaat ttt
449	Abz1mod-hIgG4 HC	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGREV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
450	Abz1mod-hKappa LC	EIVLTQSPDFQSVTPKEKVTITCRASQSIPPQFLHWYQQKPDQSPKLLIKAASQRASGVPSRESGSGSG TDFTLTINSLEAEDAATYYCHQFHSSPLTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT KSENRGEC
451	Anti-hPD-1 #1-hIgG4-L6-hIL-2 (D20A/R38E) HC Linker in dashed underline hIL-2 in	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRET ISRDNSKNTLFLQMNSLRAEDTAVYYCATNDDYWGQGTLVTVSSASTKGPSVEPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLP PSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGN KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGSAPTSSSTKKTQLQLEHLLLALQMILNGIN
	italics	*EMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCE YADETATIVEFLNRWITFCQSIISTLT*
452	Anti-hPD-1 #1-hKappa LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARESGSGSGT DFTLTISSLEPEDFAVYYCQQSSNWPRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK SENRGEC
453	OMC.1.B6-hIgG4-L6-hIL-2 (D20A/R38E) HC Linker in dashed underline hIL-2 in	EVQLLESGGGLVQPGGSLRLSCAASGFTESSNYMSWVRQAPGKGLEWVSAISSSGGTIFYADSVKGRET ISRDNSKNTLYLQMNSLRAEDTAVYYCAKHKWNAVYYDGMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV VFSCSVMHEALHNHYTQKSLSLSLGKSGGGGSAPTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLT
	italics	*NNYKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK GSETTEMCEYADETATIVEFLNRWITFCQSIISTLT*
454	OMC.2.C6-hIgG4-L6-hIL-2 (D20A/R38E) HC Linker in dashed underline hIL-2 in	EVQLLESGGGLVQPGGSLRLSCTASGFTFSSYEMQWVRQAPGKGLEWVLGITSSSSHIFYADSVKGRET VSRDNSKNTLYLQMNSLRAEDTAVYYCTKDLNSYYGLDVWGQGTTVTVSSASTKGPSVEPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHK PSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENW YVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREP QVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKS RWQEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGSAPTSSSTKKTQLQLEHLLLALQMILNGINNY
	italics	*KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFCQSIISTLT*
455	OMC.1.D6-hIgG4-L6-hIL-2 (D20A/R38E) HC Linker in dashed	EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYYMSWVRQAPGKGLEWVSAISSSGGTIFYADSVKGRFI ISRDNSKNTLYLQMNSLRAEDTAVYYCAKHKWNDVYYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
	underline hIL-2 in	REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV RWQEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGSAPTSSSTKKTQLQLEHLLLLALQMILNGINNY
	italics	*NNYKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELK GSETTEMCEYADETATIVEFLNRWITFCQSIISTLT*
456	D12-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVEPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
457	G12-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	DSLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFTI SRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTK VDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMHEALHNHYTQKSLSLSLGKA*PTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLTE KFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADET ATIVEFLNRWITFCQSIISTLT*
458	2H7-hIgG4-LE HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
459	2H7-hIgG4-LAGA HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
460	OMC.2-A3-hIgG4/A HC	EVQLLESGGCLVQPGGSLRLSCAASGFTESDYYMSWVRQAPGKGLEWVSAISSSGGTIFYADSVKGRFI ISRDNSKNTLYLQMNSLRAEDTAVYYCAKHKWNDVYYDAMDVWGQGTTVTVSSASTKGPSVEPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
461	OMC476pH7-hIgG4 HC	DMQLVESGGGVVRPGESLRLSCTASGFTFSISAMSWVRQAPGKGLEWVSAISGTAYSTYYADSVRGRET ISRDNSKNTLYLQMNSLRAEDTAVYYCAKDNFFDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLG
462	OMC476pB11.H7 LC	QSVMTQPPSASGTPGQRVTISCSGVTSNIGSNSVYWYQQLPGTAPKLLIYLNSQRPSGVPDRESGSKSG TSASLAISGLQSEDEADYYCGTWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC LISDEYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE KTVAPTECS
463	OMC476pB11-hIgG4 HC	DVQLVESGGGVVRPGESLRLSCTASGFTFSISAMSWVRQAPGKGLEWVSAISGTAYSTYYADSVRGRET ISRDNSKNTLYLQMNSLRAEDTAVYYCAKDNFFDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLG
464	OMC476pG10-hIgG4 HC	DVQLVESGGGVVRPGGSLRLSCAASGFTFSIYAMSWVRQAPGEGLEWVSHISASGGSTYYADSVKGRFA ISRDNSKNTLYLQMNSLRAEDTAVYYCTTNLGSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
		VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLG
465	OMC476pH10-hIgG4 HC	DVQLVESGGGVVRPGGSLRLSCAASGFTFSIYAVSWVRQAPGEGLEWVSHISASGGSTYYADSVKGRFA ISRDNSKNTLYLQMNSLRAEDTAVYYCTTNLGSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLG
466	OMC476pG10.H10 LC	QSVLTQPPSASGTPGQRVTISCSGSYSDIGTNYVYWYQQLPGTAPKLLIFATDRRPSGVPDRESGSKSG TSASLAISGLQSEDEADYYCGTWDDSLNVWVFGGGTKLTVLGQPKAAPSVTLEPPSSEELQANKATLVC LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE KTVAPTECS
467	OMC476pE4-hIgG4 HC	DVQLVESGGGVVRPGESLRLSCAASGFTFSTDAMGWVRQAPGEGLEWVSLISGSGYSTYYADSVKGRFT ISRDNSKNTLYLQMNSLTAEDTAVYYCAKNSLAFFDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLG
468	OMC476pE4 LC	QSVLTQPPSASGTPGQRVTISCSGGSSNIGRESVNWYQQLPGTAPKLLIYSTDRRPSGVPDRESGSKSG TSASLAISGLQSEDEADYYCGTWDNDLNGWVFGGGTKLTVLGQPKAAPSVTLEPPSSEELQANKATLVC LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE KTVAPTECS
469	J110-hIgG1 HC	DVQLQESGPGLVKPSQSLSLTCTVTGHSITSDYAWNWIRQFPGDKLEWMGYISYSGYTTYNPSLKSRVS ITRDTSKNQFFLQLNSVTTEDTATYFCARDLDYGPWFAYWGQGTLVTVSAASTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
470	J110-hKappa LC	DIQMTQSPASLSASVGETVTLTCRASENIHNYLAWYQQKQGKSPQLLVYNVKTLADGVPSRFSGSGSGT QYSLKINSLQPEDFGSYYCQHFWSSPWTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK SENRGEC
471	2H7-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLALQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
472	2H7-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTE MCEYADETATIVEFLNRWITFAQSIISTLT*
473	2H7-hIgG1-LAGA--df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVEPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTE MCEYADETATIVEFLNRWITFAQSIISTLT*

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
474	2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/I92K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVKVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
475	2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/192K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLDLQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVKVLELKGSETTE MCEYADETATIVEFLNRWITFAQSIISTLT*
476	2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/192K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLDLQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVKVLELKGSETTE MCEYADETATIVEFLNRWITFAQSIISTLT*
477	2H7-hIgG1-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRKLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
478	2H7-hIgG4-LE-df-hIL-2 (T3A/R38E/D84K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVEPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLDLQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRKLISNINVIVLELKGSETTE MCEYADETATIVEFLNRWITFAQSIISTLT*
479	2H7-hIgG4-LAGA-df-hIL-2 (T3A/R38E/D84K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLDLQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRKLISNINVIVLELKGSETTE MCEYADETATIVEFLNRWITFAQSIISTLT*
480	1H3-hIgG4-df-hIL-2 (WT) HC hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRM LTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYA DETATIVEFLNRWITFCQSIISTLT*
481	1H3-hIgG4-L6-hIL-2 (WT) HC Linker in dashed	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVEPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
	underline hIL-2 in italics	DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGS*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKN* *PKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT*
482	1H3-hIgG4 HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTESDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLG
483	1H3-hKappa-df-hIL-2 (WT) LC hIL-2 in italics	DTVLTQSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTD FTLTIDPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKFYMPKKATELKHLQCLEEEL KPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTL T*
484	1H3-hKappa-L6-hIL-2 (WT) LC Linker in dashed	DTVLTQSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTD FTLTIDPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC*SGGGGS**APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQ*
	underline hIL-2 in italics	*CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITECQ SIISTLT*
485	1H3-hIgG4-L6-hIL-2 (D20Y) HC Linker in dashed underline hIL-2 in	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKS*GGGGS**APTSSSTKKTQLQLEHLLLDLQMILNGINNYKN*
	italics	*PKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT*
486	1H3-hIgG4-df-hIL-2 (D20Y) HC hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKA*PTSSSTKKTQLQLEHLLLYLQMILNGINNYKNPKLTRM LTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYA DETATIVEFLNRWITFCQSIISTLT*
487	1H3-hIgG1-df-hIL-2 (D20Y) HC hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APTSSSTKKTQLQLEHLLLYLQMILNGINNYKNPKL TRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMC EYADETATIVEFLNRWITFCQSIISTLT*
488	1H3-hIgG4-L6-hIL-2 (D20A/R38P) HC Linker in dashed underline hIL-2 in	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKS*GGGGS**APTSSSTKKTQLQLEHLLLDLQMILNGINNYKN*
	italics	*PKLTPMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT*

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
489	1H3-hIgG4-L6-hIL-2 (D20A/R38S) HC Linker in dashed underline hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKN PKLTSMLTEKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT
490	1H3-hIgG4-L6-hIL-2 (D20A/R38D) HC Linker in dashed underline hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVEPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKN PKLTDMLTEKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT
491	1H3-hIgG4-L6-hIL-2 (D20A/R38Q/E95A) HC Linker in dashed underline hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVEPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKN PKLTQMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLALKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT
492	1H3-hIgG4-L6-hIL-2 (D20A/F42H/E95A) HC Linker in dashed underline hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKN PKLTRMLTHKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLALKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT
493	1H3-hIgG4-L6-hIL-2 (R38D/I92D) HC Linker in dashed underline hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKN PKLTDMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVDVLELKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT
494	1H3-hIgG4-L6-hIL-2 (R38E/I92D) HC Linker in dashed underline hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVEPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKN PKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVDVLELKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT
495	1H3-hIgG4-L6-hIL-2 (F42H/I92D) HC Linker in	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVEPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
	dashed	DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV
	underline	YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW
	hIL-2 in	QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGS*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKN*
	italics	*PKLTRMLTHKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVDVLELKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT*
496	1H3-hIgG4-L6-	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT
	hIL-2	ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVEPLAPCSRSTSES
	(D20A/R38E) HC	TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS
	Linker in	NTKVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV
	dashed	DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV
	underline	YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW
	hIL-2 in	QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGS*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKN*
	italics	*PKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETT FMCEYADETATIVEFLNRWITFCQSIISTLT*
497	1H3-hIgG4-L6-	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT
	hIL-2	ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVEPLAPCSRSTSES
	(T3A/D20A/	TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS
	R38E) HC	NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV
	Linker in	DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV
	dashed	YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW
	underline	QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGS*APTSSSTKKTQLQLEHLLLALQMILNGINNYKN*
	hIL-2 in	*PKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETT*
	italics	*FMCEYADETATIVEFLNRWITFCQSIISTLT*
498	1H3-hIgG4-L6-	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT
	hIL-2	ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES
	(D20A/R38E/C12	TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS
	5A) HC	NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV
	Linker in	DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV
	dashed	YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW
	underline	QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGS*APTSSSTKKTQLQLEHLLLALQMILNGINNYKN*
	hIL-2 in	*PKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETT*
	italics	*FMCEYADETATIVEFLNRWITFAQSIISTLT*
499	1H3-hIgG4-L6-	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT
	hIL-2	ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPCSRSTSES
	(T3A/D20A/R38E/	TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS
	C125A) HC	NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV
	Linker in	DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV
	dashed	YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW
	underline	QEGNVFSCSVMHEALHNHYTQKSLSLSLGKSGGGGS*APTSSSTKKTQLQLEHLLLALQMILNGINNYKN*
	hIL-2 in	*PKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETT*
	italics	*FMCEYADETATIVEFLNRWITFAQSIISTLT*
500	1H3-hIgG1-L6-	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT
	hIL-2	ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG
	(D20A/R38E) HC	TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
	Linker in	NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN
	dashed	WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
	underline	PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
	hIL-2 in	SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCEC
	italics	*YKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGS ETTEMCEYADETATIVEFLNRWITFCQSIISTLT*
501	1H3-hIgG1-L6-	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET
	hIL-2	ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG
	(T3A/D20A/R38E)	TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS
	HC	NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN
	Linker in	WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
	dashed	PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
	underline	SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCEC
	hIL-2 in	*YKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGS*
	italics	*ETTEMCEYADETATIVEFLNRWITFCQSIISTLT*
502	1H3-hIgG1-L6-	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT
	hIL-2	ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG
	(D20A/R38E/C12	TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
	5A) HC Linker in dashed underline	NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCEC
	hIL-2 in italics	*YKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNEHLRPRDLISNINVIVLELKGS ETTEMCEYADETATIVEFLNRWITFAQSIISTLT*
503	1H3-hKappa-df-hIL-2 (D20A/R38E) LC hIL-2 in italics	DTVLTQSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTD FTLTIDPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLTFKFYMPKKATELKHLQCLEEEL KPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTL T*
504	1H3-hKappa-L6-hIL-2 (D20A/R38E) LC Linker in dashed underline hIL-2 in italics	DTVLTQSPALAVSPGERVTISCRASESVRTGVHWYQQKPGQQPKLLIYGASNLESGVPARFSGSGSGTD FTLTIDPVEADDTATYFCQQSWNDPFTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGS*APTSSSTKKTQLQLEHLLLALQMILNGINN CLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITECQ SIISTLT*
505	OMC476pB11-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	DVQLVESGGGVVRPGESLRLSCTASGFTFSISAMSWVRQAPGKGLEWVSAISGTAYSTYYADSVRGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCAKDNFFDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNEHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
506	OMC476pE4-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	DVQLVESGGGVVRPGESLRLSCAASGETESTDAMGWVRQAPGEGLEWVSLISGSGYSTYYADSVKGRET ISRDNSKNTLYLQMNSLTAEDTAVYYCAKNSLAFFDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPS NTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRW QEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEM LTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYA DETATIVEFLNRWITFCQSIISTLT*
507	OMC476pG10-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	DVQLVESGGGVVRPGGSLRLSCAASGFTFSIYAMSWVRQAPGEGLEWVSHISASGGSTYYADSVKGRFA ISRDNSKNTLYLQMNSLRAEDTAVYYCTTNLGSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
508	OMC476pH10-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	DVQLVESGGGVVRPGGSLRLSCAASGFTFSIYAVSWVRQAPGEGLEWVSHISASGGSTYYADSVKGRFA ISRDNSKNTLYLQMNSLRAEDTAVYYCTTNLGSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
509	A2-hIgG4-df-hIL-2 (D20A/F42A) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRET ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLT AKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
510	A2-hIgG4-df-hIL-2 (D20A/F42S) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRET ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVEPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTRMLT SKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
511	A2-hIgG4-df-hIL-2 (D20S/R38E) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLSLQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
512	A2-hIgG4-df-hIL-2 (F42A/N88R) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT AKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISRINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
513	A2-hIgG4-df-hIL-2 (F42I/I92D) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRET ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT IKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVDVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
514	A2-hIgG4-df-hIL-2 (F42Q/I92D) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT QKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVDVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
515	A2-hIgG4-df-hIL-2 (F42T/I92D) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRET ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT TKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVDVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
516	A2-hIgG4-df-hIL-2 (F42W/I92D) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRET ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT WKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVDVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
517	A2-hIgG4-df-hIL-2 (R38E/D84K) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
		LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRKLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
518	A2-hIgG4-df-hIL-2 (R38E/192K) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVEPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVKVLELKGSETTEMCEYADE TATIVEFLNRWITFCQSIISTLT*
519	C51E6-5-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGREV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNPK LTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEM CEYADETATIVEFLNRWITFCQSIISTLT*
520	C51E6-5-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGREV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNPK LTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEM CEYADETATIVEFLNRWITFAQSIISTLT*
521	C51E6-5-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGREV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNPK LTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEM CEYADETATIVEFLNRWITFAQSIISTLT*
522	1H3-hIgG1-LAGA-L6-hIL-2 (T3A/D20A/R38E/C125A)	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSAPASSSTKKTQLQLEHLLLALQMILNGINN YKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISNINVIVLELKGS ETTFMCEYADETATIVEFLNRWITFAQSIISTLT
523	2A3-hKappa LC	EIVLTQSPGTLSLSPGERATLSCRASQSIGRSFLAWYQQKPGQAPRLLIYDASTRAADIPARFSGSGSG TDFTLTISSLEPEDFAVYYCQQYYDWPPLSFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPV TKSENRGEC
524	1H9-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCVGSGFNLKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYTRGSYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTE MCEYADETATIVEFLNRWITFCQSIISTLT*
525	1H9-hkappa LC	EIVLTQSPGTLSLSPGERATLSCRASQSIGRSFLAWYQQKPGQAPRLLIYDASTRAADIPDRESGSGSG TDFTLTINRLEPEDFAVYYCQQYYDWPPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPV TKSENRGEC

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
526	1D5-hIgG4-df-hIL-2 (D20A/R38E) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCVGSGENFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYTRGSYFYDAMDVWGQGTTVTVSSASTKGPSVEPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APTSSSTKKTQLQLEHLLLALQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTE MCEYADETATIVEFLNRWITFCQSIISTLT*
527	1D5-hKappa LC	EIVLTQSPGTLSLSPGERATLSCRASQSIGRSFLAWYQQKPGQAPRLLIYDASTRATDIPDRESGSGSG TEFTLTISSLQSEDFAVYYCQQYYDWPPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPV TKSENRGEC
528	1D5-hIgG4-LE-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCVGSGENFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYTRGSYFYDAMDVWGQGTTVTVSSASTKGPSVEPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTE MCEYADETATIVEFLNRWITFAQSIISTLT*
529	1D5-hIgG4-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCVGSGENFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYTRGSYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTE MCEYADETATIVEFLNRWITFAQSIISTLT*
530	2H7-hIgG1-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLALQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
531	2H7-hIgG1-LE-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLALQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
532	H7-767 HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFKSYAMHWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYDRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTIMISRTPEVTCVVVDVSHEDP EVKENWYVDGVEVHNAKIKPREEQYNSTYRVVSVLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVESCSVMHEALHNHYTQKSISLSPGKAPASSSTKKTQLQLEHLLLALQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHIRPRDLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT
533	2H7-hIgG1-LE-df-hIL-2 (T3A/R38E/D84K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRKLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
534	2H7-hIgG4-df-hIL-2 (T3A/R38E/D84K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVEPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLDLQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRKLISNINVIVLELKGSETTE MCEYADETATIVEFLNRWITFAQSIISTLT*
535	2H7-hIgG1-df-hIL-2 (T3A/R38E/192K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVKVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
536	2H7-hIgG1-LE-df-hIL-2 (T3A/R38E/192K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELEGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVKVLELKGSE TTEMCEYADETATIVEFLNRWITFAQSIISTLT*
537	2H7-hIgG4-df-hIL-2 (T3A/R38E/192K/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVEPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLDLQMILNGINNYKNP KLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVKVLELKGSETTF MCEYADETATIVEFLNRWITFAQSIISTLT*
538	2H7-hIgG1-LAGA-df-hIL2 (T3A/D20S/R38E/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLSLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE TTEMCEYADETATIVEFLNRWITFAQSIISTLT*
539	2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/D84F/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKENWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRFLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
540	2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/I92R/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVRVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
541	2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/I92E/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVEVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
542	2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/192S/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVSVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
543	2H7-hIgG1-LAGA-df-hIL2 (T3A/R38E/I92D/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVDVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
544	2H7-hIgG1-LAGA-df-hIL2 (T3A/H16E/R38E/C125A) HC hIL-2 in italics	EVQLLESGGGLVQPGGSLRLSCAASGFTFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNNLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEELLLDLQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT*
545	1H3-hIgG1-L6-hIL-2 (T3A/D20A/R38E/C125A) HC Linker in dashed underline	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCEC
	hIL-2 in italics	*YKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGS ETTEMCEYADETATIVEFLNRWITFAQSIISTLT*
546	1H3-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNPKL TEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMC EYADETATIVEFLNRWITFAQSIISTLT*
547	C51E6-5-hIgG4/k-LE HC	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGREV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
548	C51E6-5-hIgG4/k-LAGA HC	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGREV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVEPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
549	C51E6-5-hIgG4/k-LEPG HC	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGREV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLGSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
550	C51E6-5-hIgG4/k-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGREV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVEPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNPK LTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEM CEYADETATIVEFLNRWITFAQSIISTLT*
551	C51E6-5-hIgG4/k-LEPG-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	QVQLVQSGSELKKPGASVKVSCKASGYSLYGTSMHWVRQAPGQGLEWMGYISPFTGRATYAQGFTGRFV FSLDTSVSTAYLQISSLKAEDTAVYYCARDYDYRYYYAMDYWGQGTTVTVSSASTKGPSVEPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVESKYGPPCPPCPAPEFEGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLGSSIEKTISKAKGQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNPK LTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEM CEYADETATIVEFLNRWITFAQSIISTLT*
552	A2-hIgG4/k-LE HC	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVEPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFeGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLG
553	A2-hIgG4/k-LAGA HC	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFaGaPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLG
554	A2-hIgG4/k-LEPG HC	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRET ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFeGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLgSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLG
555	A2-hIgG4/k-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRET ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFAQSIISTLT*

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
556	A2-hIgG4/k-LE-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRET ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFEGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFAQSIISTLT*
557	A2-hIgG4/k-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRET ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFAQSIISTLT*
558	A2-hIgG4/k-LEPG-df-hIL-2 (T3A/D20A/R38E/C125A) HC hIL-2 in italics	DVQLVESGGGLVQPGGSLRLSCAASGFTFDISAMSWVRQAPGKGLEWVSTISGSAYSTYYADSVKGRFT ISRDNSKSTLYLQMNSLRAEDTAVYYCAREIFSDYWGLGTLVTVSSASTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPPCPAPEFEGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLGSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLSLGK*APASSSTKKTQLQLEHLLLALQMILNGINNYKNPKLTEMLT FKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNEHLRPRDLISNINVIVLELKGSETTEMCEYADE TATIVEFLNRWITFAQSIISTLT*
559	Anti-hPD-1 #1 HC	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKGLEWVAVIWYDGSKRYYADSVKGRET ISRDNSKNTLFLQMNSLRAEDTAVYYCATNDDYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKV DKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQENWYVDGVE VHNAKTKPREEQFNSTYRVVSVLIVLHQDWINGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLP PSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLG
560	Anti-CD20-hIgG1/k HC	QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKEKGKAT LTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVSAASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
561	Anti-CD20-hIgG1/k-LAGA HC	QVQLQQPGAELVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPGNGDTSYNQKEKGKAT LTADKSSSTAYMQLSSLTSEDSAVYYCARSTYYGGDWYFNVWGAGTTVTVSAASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
562	Anti-CD20-hKappa LC	QIVLSQSPAILSASPGEKVTMTCRASSSVSYIHWFQQKPGSSPKPWIYATSNLASGVPVRESGSGSGTS YSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS ENRGEC
563	1H3-hIgG1-LAGA-df-hIL-2 (T3A/C125A) HC hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAVSGFTESDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK*APASSSTKKTQLQLEHLLLLDLQMILNGINNYKNPKL TRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMC EYADETATIVEFLNRWITFAQSIISTLT*

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
564	anti-mPD-1 RMP1-14 mIgG2b-N297A HC	EVQLQESGPGLVKPSQSLSLTCSVTGYSITSSYRWNWIRKFPGNRLEWMGYINSAGISNYNPSLKRRIS ITRDTSKNQFFLQVNSVTTEDAATYYCARSDNMGTTPFTYWGQGTLVTVSSAKTTPPSVYPLAPGCGDT TGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHP ASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVS EDDPDVQISWFVNNVEVHTAQTQTHREDYASTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTI SKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGENPGDISVEWTSNGHTEENYKDTAPVLDSDGSYF IYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
565	anti-mPD-1 RMP1-14 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) HC linker in dashed underline hIL-2 in italics	EVQLQESGPGLVKPSQSLSLTCSVTGYSITSSYRWNWIRKFPGNRLEWMGYINSAGISNYNPSLKRRIS ITRDTSKNQFFLQVNSVTTEDAATYYCARSDNMGTTPFTYWGQGTLVTVSSAKTTPPSVYPLAPGCGDT TGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHP ASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVS EDDPDVQISWFVNNVEVHTAQTQTHREDYASTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTI SKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGENPGDISVEWTSNGHTEENYKDTAPVLDSDGSYF SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSAPASSSTKKTQLQLEHLLLALQMILNGINN *QMILNGINNYKNPKLTRMLTKKERMPKKATELKHLQCLEEELKPLEERLNLAQSKNFHLRPRDLISNIN VIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT*
566	anti-mPD-1 RMP1-14 mKappa LC	DIVMTQGTLPNPVPSGESVSITCRSSKSLLYSDGKTYLNWYLQRPGQSPQLLIYWMSTRASGVSDRESG SGSGTDFTLKISGVEAEDVGIYYCQQGLEFPTFGGGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVC FLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTS PIVKSENRNEC
567	anti-mPD-1 RMP1-30 mIgG2b-N297A HC	EVQLVESGGGLVQPGRSLKLSCAASGFTFGDYSMAWVRQAPKRGLEWVANIIYDGSRTFYRDSVKGRFT ISRDNAKPTLYLQMDSLRPEDTATYYCATHNYPGYAMEAWGQGTSVTVSSAKTTPPSVYPLAPGCGDTT GSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPA SSTTVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSE DDPDVQISWFVNNVEVHTAQTQTHREDYASTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTIS KIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGENPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK
568	anti-mPD-1 RMP1-30 mKappa LC	DTVLTQSPALPVSLGQRVNISCRATKSVSRYVHWYQQKSGQQPRLLIYTTSNLESGVPSRFSGSGSGTD FTLTIDPVEADDIANYYCQQSNEIPYTFGAGTKLELKRADAAPTVSIFPPSSEQLTSGGASVVCELNNE YPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS ENRNEC
569	anti-mPD-1 RMP1-30 mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) HC linker in dashed underline hIL-2 in italics	EVQLVESGGGLVQPGRSLKLSCAASGFTFGDYSMAWVRQAPKRGLEWVANITYDGSRTFYRDSVKGRFT ISRDNAKPTLYLQMDSLRPEDTATYYCATHNYPGYAMEAWGQGTSVTVSSAKTTPPSVYPLAPGCGDTT GSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPA SSTTVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSE DDPDVQISWFVNNVEVHTAQTQTHREDYASTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTIS KIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGENPGDISVEWTSNGHTEENYKDTAPVLDSDGSYF IYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGKSGGGGSAPTSSSTKKTQLQLEHLLLDL *MILNGINNYKNPKLTRMLTKKFrMPKKATELKHLQCLEEELKPLEErLNLAQSKNFHLRPRDLISNINV IVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT*
570	anti-KLH-C3-mIgG2b-N297A-L6-hIL-2 (F42K/Y45R/V69R) HC linker in dashed underline hIL-2 in italics	EVQLVGSGGGLVQPGGSLKLSCAASGFTFSDFYMAWVRQAPTKGLEWVASISTGGGNTHYRDSVKGRFT ISRDNAKSTLYLQMDSLRSEETATYYCARLLSTISTPFDYWGQGVIVTVSSAKTTPPSVYPLAPGCGDT TGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHP ASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVS EDDPDVQISWFVNNVEVHTAQTQTHREDYASTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTI SKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGENPGDISVEWTSNGHTEENYKDTAPVLDSDGSYF IYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGKSGGGGSAPTSSSTKKTQLQLEHLLLDL *QMILNGINNYKNPKLTRMLTKKFrMPKKATELKHLQCLEEELKPLEErLNLAQSKNFHLRPRDLISNIN VIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT*
571	KLH-C3-mKappa LC	DVVLIQSPTTLSVTPGETVSLSCRASHSVGTNLHWYQQRTNESPSLLIKYSSHSTSGIPSRESATGSGT DFTLNISNVEFDDVASYFCQQSQKWPLTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCELNN FYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVK SENRNEC

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
572	2D12-hIgG1-L6-hIL-2 HC linker in dashed underline hIL-2 in italics	EVQLQQSGPELVKPGASVKISCKTSGYTFTEYTMHWVKQSHGKSLEWIGGINPNNGGTTYNQKFKGKAT LTVDKSSSTAYMELRSLTSQDSAVYYCARDYYRYGHYYAMDYWGQGTSVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGKSGGGGSAPTSSSTKKTQLQLEHLLLDLQ
		NGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVL ELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
573	2D12-hKappa LC	QIVLTQSPAIMSASPGEKVTMTCSVSSSVREMHWYQQKSGTSPKRWIYDTSKLASGVPARFSGSGSGTS YSLTISSMEAEDAATYYCQQWSSNPPTFGGGTKLKIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNE YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS FNRGEC
574	hIL-2 F42A/Y45A/L72G	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLT**A**KF**A**MPKKATELKHLQCLEEELKPLEEV LN**G**AQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
575	hIL-2 H16A/F42A	APTSSSTKKTQLQLE**A**LLLDLQMILNGINNYKNPKLTRMLT**A**KFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
576	1H9-hIgG4 HC	EVQLLESGGGLVQPGGSLRLSCVGSGFNLKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYTRGSYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
577	1D5-hIgG4 HC	EVQLLESGGGLVQPGGSLRLSCVGSGENFKDYCMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRET ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYTRGSYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQ FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQP REPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTV DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
578	Anti-hPD-1 #2 HC	QVQLVQSGVEVKKPGASVKVSCKASGYTFTNYYMYWVRQAPGQGLEWMGGINPSNGGTNFNEKFKNRVT LTTDSSTTAYMELKSLQFDDTAVYYCARRDYRFDMGFDYWGQGTTVTVSSASTKGPSVFPLAPCSRST SESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDH KPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFN WYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWINGKEYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDK SRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
579	Anti-hPD-1 #2 LC	EIVLTQSPATLSLSPGERATLSCRASKGVSTSGYSYLHWYQQKPGQAPRLLIYLASYLESGVPARFSGS GSGTDFTLTISSLEPEDFAVYYCQHSRDLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC LINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS PVTKSENRGEC
580	human PD-1 receptor lentiviral vector	gtcgacggatcgggagatctcccgatcccctatggtgcactctcagtacaatctgctctgatgccgcat agttaagccagtatctgctccctgcttgtgtgttggaggtcgctgagtagtgcgcgagcaaaatttaag ctacaacaaggcaaggcttgaccgacaattgcatgaagaatctgcttagggttaggcgttttgcgctgc ttcgcgatgtacgggccagatatacgcgttgacattgattattgactagttattaatagtaatcaatta cggggtcattagttcatagcccatatatggagttccgcgttacataacttacggtaaatggcccgcctg gctgaccgcccaacgacccccgcccattgacgtcaataatgacgtatgttcccatagtaacgccaatag ggactttccattgacgtcaatgggtggagtatttacggtaaactgcccacttggcagtacatcaagtgt atcatatgccaagtacgcccccctattgacgtcaatgacggtaaatggcccgcctggcattatgcccagt acatgaccttatgggactttcctacttggcagtacatctacgtattagtcatcgctattaccatggtga tgcggttttggcagtacatcaatgggcgtggatagcggtttgactcacggggatttccaagtctccacc ccattgacgtcaatgggagtttgttttggcaccaaaatcaacgggactttccaaaatgtcgtaacaact ccgccccattgacgcaaatgggcggtaggcgtgtacggtgggaggtctatataagcagcgcgttttgcc tgtactgggtctctctggttagaccagatctgagcctgggagctctctggctaactagggaacccactg cttaagcctcaataaagcttgccttgagtgcttcaagtagtgtgtgcccgtctgttgtgtgactctggt aactagagatccctcagacccttttagtcagtgtggaaaatctctagcagtggcgcccgaacagggact tgaaagcgaaagggaaaccagaggagctctctcgacgcaggactcggcttgctgaagcgcgcacggcaa gaggcgaggggcggcgactggtgagtacgccaaaaattttgactagcggaggctagaaggagagagatg ggtgcgagagcgtcagtattaagcgggggagaattagatcgcgatgggaaaaaattcggttaaggccag ggggaaagaaaaaatataaattaaaacatatagtatgggcaagcagggagctagaacgattcgcagtta atcctggcctgttagaaacatcagaaggctgtagacaaatactgggacagctacaaccatcccttcaga caggatcagaagaacttagatcattatataatacagtagcaaccctctattgtgtgcatcaaaggatag agataaaagacaccaaggaagctttagacaagatagaggaagagcaaaacaaaagtaagaccaccgcac agcaagcggccgctgatcttcagacctggaggaggagatatgagggacaattggagaagtgaattatat

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
		aaatataaagtagtaaaaattgaaccattaggagtagcacccaccaaggcaaagagaagagtggtgcag
		agagaaaaaagagcagtgggaataggagctttgttccttgggttcttgggagcagcaggaagcactatg
		ggcgcagcgtcaatgacgctgacggtacaggccagacaattattgtctggtatagtgcagcagcagaac
		aatttgctgagggctattgaggcgcaacagcatctgttgcaactcacagtctggggcatcaagcagctc
		caggcaagaatcctggctgtggaaagatacctaaaggatcaacagctcctggggatttggggttgctct
		ggaaaactcatttgcaccactgctgtgccttggaatgctagttggagtaataaatctctggaacagatt
		tggaatcacacgacctggatggagtgggacagagaaattaacaattacacaagcttaatacactcctta
		attgaagaatcgcaaaaccagcaagaaaagaatgaacaagaattattggaattagataaatgggcaagt
		ttgtggaattggtttaacataacaaattggctgtggtatataaaattattcataatgatagtaggaggc
		ttggtaggtttaagaatagtttttgctgtactttctatagtgaatagagttaggcagggatattcacca
		ttatcgtttcagacccacctcccaaccccgaggggacccgacaggcccgaaggaatagaagaagaaggt
		ggagagagagacagagacagatccattcgattagtgaacggatcggcactgcgtgcgccaatttctgcag
		acaaatggcagtattcatccacaattttaaaagaaaaggggggattgggggtacagtgcaggggaaag
		aatagtagacataatagcaacagacatacaaactaaagaattacaaaaacaaattacaaaaattcaaaa
		ttttcgggtttattacagggacagcagagatccagtttggttaattaagtaattcgctagctaggtctt
		gaaaggagtgggaattggctccggtgcccgtcagtgggcagagcgcacatcgcccacagtccccgagaa
		gttgggggggaggggtcggcaattgatccggtgcctagagaaggtggcgcggggtaaactgggaaagtga
		tgtcgtgtactggctccgccttttcccgagggtgggggagaaccgtatataagtgcagtagtcgccgt
		gaacgttctttttcgcaacgggtttgccgccagaacacaggaccggttctagagcgctgccaccatgca
		gatcccacaggcgccctggccagtcgtctgggcggtgctacaactgggctggcggccaggatggttctt
		agactccccagacaggccctggaacccccccaccttctccccagccctgctcgtggtgaccgaaggggа
		caacgccaccttcacctgcagcttctccaacacatcggagagcttcgtgctaaactggtaccgcatgag
		ccccagcaaccagacggacaagctggccgccttccccgaggaccgcagccagccccggccaggactgccg
		cttccgtgtcacacaactgcccaacgggcgtgacttccacatgagcgtggtcagggcccggcgcaatga
		cagcggcacctacctctgtggggccatctccctggccccccaaggcgcagatcaaagagagcctgcgggc
		agagctcagggtgacagagagaagggcagaagtgcccacagcccaccccagcccctcacccaggccagc
		cggccagttccaaaccctggtggttggtgtcgtgggcggcctgctgggcagcctggtgctgctagtctg
		ggtcctggccgtcatctgctcccgggccgcacgagggacaataggagccaggcgcaccggccagcccct
		gaaggaggacccctcagccgtgcctgtgttctctgtggactatggggagctggatttccagtggcgaga
		gaagaccccggagccccccgtgccctgtgtccctgagcagacggagtatgccaccattgtctttcctag
		cggaatgggcacctcatccccgcccgcaggggctcagctgacggccctcggagtgcccagccactgag
		gcctgaggatggacactgctcttggcccctctgagcccctctccctccccccccctaacgttactggcc
		gaagccgcttggaataaggccggtgtgcgtttgtctatatgttatttccaccatattgccgtcttttg
		gcaatgtgagggcccggaaacctggccctgtcttcttgacgagcattcctaggggtctttcccctctcg
		ccaaaggaatgcaaggtctgttgaatgtcgtgaaggaagcagttcctctggaagcttcttgaagacaaa
		caacgtctgtagcgaccctttgcaggcagcggaacccccacctggcgacaggtgcctctgcggccaaa
		agccacgtgtataagatacacctgcaaaggcggcacaaccccagtgccacgttgtgagttggatagttg
		tggaaagagtcaaatggctctcctcaagcgtattcaacaaggggctgaaggatgcccagaaggtacccc
		attgtatgggatctgatctggggcctcggtgcacatgctttacatgtgtttagtcgaggttaaaaaaac
		gtctaggccccccgaaccacggggacgtggttttcctttgaaaaacacgatgataatatggccacaatg
		accgagtacaagccacggtgcgcctcgccacccgcgacgacgtccccagggccgtacgcaccctcgcc
		gccgcgttcgccgactaccccgccacgcgccacaccgtcgatccggaccgccacatcgagcgggtcacc
		gagctgcaagaactcttcctcacgcgcgtcgggctcgacatcggcaaggtgtgggtcgcggacgacggc
		gccgcggtggcggtctggaccacgccggagagcgtcgaagcgggggcggtgttcgccgagatcggcccg
		cgcatggccgagttgagcggttcccggctggccgcgcagcaacagatggaaggcctcctggcgccgcac
		cggcccaaggagcccgcgtggttcctggccaccgtcggagtctcgcccgaccaccagggcaagggtctg
		ggcagcgccgtcgtgctccccggagtggaggcggccgagcgcgccggggtgcccgccttcctggagacc
		tccgcgccccgcaacctccccttctacgagcggctcggcttcaccgtcaccgccgacgtcgaggtgccc
		gaaggaccgcgcacctggtgcatgacccgcaagcccggtgcctgaacgcgttaagtcgacaatcaacct
		ctggattacaaaatttgtgaaagattgactggttattcttaactatgttgctcctttttacgctatgtgga
		tacgctgctttaatgcctttgtatcatgctattgcttcccgtatggctttcattttctcctccttgtat
		aaatcctggttgctgtctctttatgaggagttgtggcccgttgtcaggcaacgtggcgtggtgtgcact
		gtgtttgctgacgcaacccccactggttggggcattgccaccacctgtcagctcctttccgggactttc
		gctttcccctccctattgccacggcggaactcatcgccgcctgccttgcccgctgctggacaggggct
		cggctgttgggcactgacaattccgtggtgttgtcggggaaatcatcgtcctttccttggctgctcgcc
		tgtgttgccacctggattctgcgcgggacgtccttctgctacgtcccttcggccctcaatccagcggac
		cttccttcccgcggcctgctgccggctctgcggcctcttccgcgtcttcgccttcgccctcagacgagt
		cggatctccctttgggccgcctccccgcgtcgacttaagaccaatgacctacaaggcagctgtagatc
		ttagccactttttaaaagaaaaggggggactggaagggctaattcactcccaacgaagacaagatctgc
		tttttgcttgtactgggtctctctggttagaccagatctgagcctgggagctctctggctaactaggga
		acccactgcttaagcctcaataaagcttgccttgagtgcttcaagtagtgtgtgcccgtctgttgtgtg
		actctggtaactagagatccctcagacccttttagtcagtgtggaaaatctctagcagggcccgttaa
		acccgctgatcagcctcgactgtgccttctagttgccagccatctgttgtttgcccctcccccgtgcct
		tccttgaccctggaaggtgccactcccactgtccttcctaataaaatgaggaaattgcatcgcattgt
		ctgagtaggtgtcattctattctggggggtggggtggggcaggacagcaaggggaggattgggaagac
		aatagcaggcatgctggggatgcggtgggctctatggcttctgaggcggaaagaaccagctggggctct
		aggggtatccccacgcgccctgtagcggcgcattaagcgcggcgggtgtggtggttacgcgcagcgtg
		accgctacacttgccagcgccctagcgcccgctcctttcgctttcttcccttcctttctcgccacgttc
		gccggctttccccgtcaagctctaaatcgggggctccctttagggttccgatttagtgctttacggcac
		ctcgaccccaaaaaacttgattagggtgatggttcacgtagtgggccatcgccctgatagacggtttttt
		cgccctttgacgttggagtccacgttctttaatagtggactcttgttccaaactggaacaacactcaac
		cctatctcggtctattcttttgatttataagggattttgccgatttcggcctattggttaaaaaatgag
		ctgatttaacaaaaatttaacgcgaattaattctgtggaatgtgtgtcagttagggtgtggaaagtccc
		caggctccccagcaggcagaagtatgcaaagcatgcatctcaattagtcagcaaccaggtgtggaaagt
		ccccaggctccccagcaggcagaagtatgcaaagcatgcatctcaattagtcagcaaccatagtcccgc

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
		ccctaactccgcccatcccgcccctaactccgcccagttccgcccattctccgccccatggctgactaa ttttttttatttatgcagaggccgaggccgcctctgcctctgagctattccagaagtagtgaggaggct tttttggaggcctaggcttttgcaaaaagctcccgggagcttgtatatccatttcggatctgatcagc acgtgttgacaattaatcatcggcatagtatatcggcatagtataatacgacaaggtgaggaactaaac catggccaagttgaccagtgccgttccggtgctcaccgcgcgcgacgtcgccggagcggtcgagttctg gaccgaccggctcgggttctcccgggacttcgtggaggacgacttcgccggtgtggtccgggacgacgt gaccctgttcatcagcgcggtccaggaccaggtggtgccggacaacaccctggcctgggtgtgggtgcg cggcctggacgagctgtacgccgagtggtcggaggtcgtgtccacgaacttccgggacgcctccgggcc ggccatgaccgagatcggcgagcagccgtgggggcgggagttcgccctgcgcgacccggccggcaactg cgtgcacttcgtggccgaggagcaggactgacacgtgctacgagatttcgattccaccgccgccttcta tgaaaggttgggcttcggaatcgttttccgggacgccggctggatgatcctccagcgcggggatctcat gctggagttcttcgcccaccccaacttgtttattgcagcttataatggttacaaataaagcaatagcat cacaaatttcacaaataaagcatttttttcactgcattctagttgtggtttgtccaaactcatcaatgt atcttatcatgtctgtataccgtcgacctctagctagagcttggcgtaatcatggtcatagctgtttcc tgtgtgaaattgttatccgctcacaattccacacaacatacgagccggaagcataaagtgtaaagcctg gggtgcctaatgagtgagctaactcacattaattgcgttgcgctcactgcccgctttccagtcgggaaa cctgtcgtgccagctgcattaatgaatcggccaacgcgcggggagaggcggtttgcgtattgggcgctc ttccgcttcctcgctcactgactcgctgcgctcggtcgttcggctgcggcgagcggtatcagctcactc aaaggcggtaatacggttatccacagaatcaggggataacgcaggaaagaacatgtgagcaaaaggcca gcaaaaggccaggaaccgtaaaaaggccgcgttgctggcgtttttccataggctccgccccccctgacga gcatcacaaaaatcgacgctcaagtcagaggtggcgaaacccgacaggactataaagataccaggcgtt tcccccctggaagctccctcgtgcgctctcctgttccgaccctgccgcttaccggatacctgtccgcctt tctcccttcgggaagcgtggcgctttctcatagctcacgctgtaggtatctcagttcggtgtaggtcgt tcgctccaagctgggctgtgtgcacgaaccccccgttcagcccgaccgctgcgccttatccggtaacta tcgtcttgagtccaacccggtaagacacgacttatcgccactggcagcagccactggtaacaggattag cagagcgaggtatgtaggcggtgctacagagttcttgaagtggtggcctaactacggctacactagaag aacagtatttggtatctgcgctctgctgaagccagttaccttcggaaaaagagttggtagctcttgatc cggcaaacaaaccaccgctggtagcggtggttttttttgtttgcaagcagcagattacgcgcagaaaaaa aggatctcaagaagatcctttgatcttttctacggggtctgacgctcagtggaacgaaaactcacgtta agggattttggtcatgagattatcaaaaaggatcttcacctagatccttttaaattaaaaatgaagttt taaatcaatctaaagtatatatgagtaaacttggtctgacagttaccaatgcttaatcagtgaggcacc tatctcagcgatctgtctatttcgttcatccatagttgcctgactccccgtcgtgtagataactacgat acgggagggcttaccatctggccccagtgctgcaatgataccgcgagacccacgctcaccggctccaga tttatcagcaataaaccagccagccggaagggccgagcgcagaagtggtcctgcaactttatccgcctc catccagtctattaattgttgccgggaagctagagtaagtagttcgccagttaatagtttgcgcaacgt tgttgccattgctacaggcatcgtggtgtcacgctcgtcgtttggtatggcttcattcagctccggttc ccaacgatcaaggcgagttacatgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctcc gatcgttgtcagaagtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctct tactgtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctgagaata gtgtatgcggcgaccgagttgctcttgcccggcgtcaatacgggataataccgcgccacatagcagaac tttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactctcaaggatcttaccgctgttgag atccagttcgatgtaacccactcgtgcacccaactgatcttcagcatcttttactttcaccagcgtttc tgggtgagcaaaaacaggaaggcaaaatgccgcaaaaaagggaataagggcgacacggaaatgttgaat actcatactcttcctttttcaatattattgaagcatttatcagggttattgtctcatgagcggatacat atttgaatgtatttagaaaaataaacaaatagggggttccgcgcacatttccccgaaaagtgccacctga c
581	hIL-2 V69R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEE**R** LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
582	H7-02-hIgG1-LAGA-df-hIL-2 (T3A/D20A/R38E/C125A) HC	EVQLLESGGGLVQPGGSLRLSCAASGFTFKSYAMTWVRQAPGKGLEWVSAIVYSGGSTYYADSVKGRFT ISRDNSKNTLYLQMNSLRAEDTAVYYCAKYTRASYFYDAMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGAPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKAPASSSTKKTQLQLEHLLLALQMILNGINNY KNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSE TTFMCEYADETATIVEFLNRWITFAQSIISTLT
583	H7-02-hKappa LC	EIVLTQSPGTLSLSPGERATLSCRASQSISSSFLAWYQQKPGQAPRLLIYDASTRATGIPDRESGSGSG TDFTLTISRLEPEDFAVYYCQQYYDWPPLSFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPV TKSENRGEC
584	hPD-L1	MRIFAVEIFMTYWHLLNAFTVTVPKDLYVVEYGSNMTIECKFPVEKQLDLAALIVYWEMEDKNIIQFVH GEEDLKVQHSSYRQRARLLKDQLSLGNAALQITDVKLQDAGVYRCMISYGGADYKRITVKVNAPYNKIN QRILVVDPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLENVTSTLRINTTTNEIE YCTFRRLDPEENHTAELVIPELPLAHPPNERTHLVILGAILLCLGVALTFIERLRKGRMMDVKKCGIQD TNSKKQSDTHLEET
585	KLH-C3-hIgG4 HC	EVQLVGSGGGLVQPGGSIKLSCAASGFTFSDFYMAWVRQAPTKGLEWVASISTGGGNTHYRDSVKGRFT ISRDNAKSTLYLQMDSLRSEETATYYCARLISTISTPFDYWGQGVIVTVSSASTKGPSVEPLAPCSRST SESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTKTYTCNVDH KPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQEN

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
		WYVDGVEVHNAKTKPREEQENSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPRE PQVYTIPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDK SRWQEGNVESCSVMHEALHNHYTQKSLSLSLGK
586	KLH-C3-hKappa LC	DVVLIQSPTTLSVTPGETVSLSCRASHSVGTNLHWYQQRTNESPSLLIKYSSHSTSGIPSRFSATGSGT DETINISNVEFDDVASYFCQQSQKWPLTFGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLINN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK SENRGEC
587	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (E15A) HC	EVQLVESGGGLVQPGRSLKLSCAVSGETESDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVEPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVESCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLAHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWI TFCQSIISTLT
588	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (D20I) HC	EVQLVESGGGLVQPGRSLKLSCAVSGETESDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGERRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS IPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICISGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLILQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTET
589	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (D20S) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLSLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT
590	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (D20H) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTESDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTIPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVESCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLHLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT
591	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (D20W) HC	EVQLVESGGGLVQPGRSIKLSCAVSGETFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGFRRIKSGSLYMLCIGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLWLQMILNGINNYKNPKLTRMLTEKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWI TFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
592	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (D20Y) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLYLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT
593	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (D20R) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVEPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLRLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVENLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWI TFCQSIISTLT
594	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (D20F) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALISGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKITVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGERRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLFLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWI TFCQSIISTIT
595	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (D84K) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTIPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRKLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT
596	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (S87A) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTESDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTIPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLIANINVIVLELKGSETTEMCEYADETATIVEFLNRWI TFCQSIISTLT
597	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (N88Y) HC	EVQLVESGGGLVQPGRSLKLSCAVSGETESDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYEDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKITVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
		GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTEKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISYINVIVLELKGSETTEMCEYADETATIVEFLNRWI IFCQSIISTIT
598	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (N88D) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVESCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISDINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT
599	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (N88R) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISRINVIVLELKGSETTEMCEYADETATIVEFLNRWI TFCQSIISTLT
600	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (N88E) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTESDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDSDGSFFLYSKITVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGERRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS IPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISEINVIVLELKGSETTEMCEYADETATIVEFLNRWI TFCQSIISTIT
601	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (N88F) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVESCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISFINVIVLELKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT
602	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (N88I) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMLNCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISIINVIVLELKGSETTEMCEYADETATIVEFLNRWI TFCQSIISTLT
603	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (I92A) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRET ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
		SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGERRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGGGGGSGGGSAPTSSSTKKTQLQLEHLLIDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVINLAQSKNFHLRPRDLISNINVAVIELKGSETTEMCEYADETATIVEFLNRWI TFCQSIISTIT
604	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (E95A) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVESCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLALKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT
605	1H3-hIgG1-L6-hCD25 (1-164)-L20-hIL-2 (E95K) HC	EVQLVESGGGLVQPGRSLKLSCAVSGFTFSDYAMAWVRQAPKKGLEWVATISYDGSRTYYRDSVKGRFT ISRDNAKITLYLQMDSLRSEDTATYYCARHGSGYFDYWGQGVMVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKEN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLIVLHQDWINGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKSGGGGSELCDDDPPEIPHATFKAMAYKEGTMINCEC KRGFRRIKSGSLYMLCTGNSSHSSWDNQCQCTSSATRNTTKQVTPQPEEQKERKTTEMQSPMQPVDQAS LPGHCREPPPWENEATERIYHFVVGQMVYYQCVQGYRALHRGPAESVCKMTHGKTRWTQPQLICTSGGG GSGGGGSGGGGSGGGSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATEL KHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLKLKGSETTFMCEYADETATIVEFLNRWI TFCQSIISTLT
606	hIL-2 D20R/R38E	APTSSSTKKTQLQLEHLLL**R**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
607	hIL-2 D20N/R38E	APTSSSTKKTQLQLEHLLL**N**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
608	hIL-2 D20Q/R38E	APTSSSTKKTQLQLEHLLL**Q**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
609	hIL-2 D20E/R38E	APTSSSTKKTQLQLEHLLL**E**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
610	hIL-2 D20G/R38E	APTSSSTKKTQLQLEHLLL**G**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
611	hIL-2 D20I/R38E	APTSSSTKKTQLQLEHLLL**I**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
612	hIL-2 D20L/R38E	APTSSSTKKTQLQLEHLLL**L**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
613	hIL-2 D20K/R38E	APTSSSTKKTQLQLEHLLL**K**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
614	hIL-2 D20M/R38E	APTSSSTKKTQLQLEHLLL**M**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
615	hIL-2 D20F/R38E	APTSSSTKKTQLQLEHLLL**F**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
616	hIL-2 D20P/R38E	APTSSSTKKTQLQLEHLLL**P**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
617	hIL-2 D20T/R38E	APTSSSTKKTQLQLEHLLL**T**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFCQSIISTLT
618	hIL-2 D20W/R38E	APTSSSTKKTQLQLEHLLL**W**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
619	hIL-2 D20Y/R38E	APTSSSTKKTQLQLEHLLL**Y**LQMILNGINNYKNPKLT**E**MLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT

TABLE 29-continued

Sequences

SEQ ID NO:	Name	Sequence
620	hIL-2 D20V/R38E	APTSSSTKKTQLQLEHLLLVLQMILNGINNYKNPKLTEMLTFKFYMPKKATELKHLQCLEEELKPLEEV LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT
621	hIL-2 F42K/Y45R/V69R	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTKKFRMPKKATELKHLQCLEEELKPLEER LNLAQSKNFHLRPRDLISNINVIVLELKGSETTEMCEYADETATIVEFLNRWITFCQSIISTLT

EMBODIMENTS

The following list of embodiments is intended to complement, rather than displace or supersede, the previous descriptions.

Embodiment 1. A modified human interleukin-2 (hIL-2) protein, comprising a substitution at amino acid position 20 and a substitution at amino acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345, wherein the modified hIL-2 protein exhibits reduced potency on both a high affinity hIL-2 receptor and on an intermediate affinity hIL-2 receptor relative to a non-modified hIL-2.

Embodiment 2. The modified hIL-2 protein of embodiment 1, wherein the substitution at amino acid position 20 is selected from a D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitution.

Embodiment 3. The modified hIL-2 protein of embodiment 1 or 2, wherein the substitution at amino acid position 38 is selected from an R38E, R38N, R38G, R38H, R38I, R38L, R38M, R38F, R38P, R38S, R38T, R38W, R38Y, R38V, R38A, R38Q, R38D, and R38K substitution.

Embodiment 4. The modified hIL-2 protein of any one of the previous embodiments, further comprising a deletion or substitution at amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Embodiment 5. The modified hIL-2 protein of embodiment 4, wherein the substitution at amino acid position 3 is T3A.

Embodiment 6. The modified hIL-2 protein of any one of the previous embodiments, further comprising a deletion or substitution at amino acid position 125 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Embodiment 7. The modified hIL-2 protein of embodiment 6, wherein the substitution at amino acid position 125 is C125A.

Embodiment 8. The modified hIL-2 protein of any one of the previous embodiments, wherein the modified hIL-2 protein exhibits about a 1,000-fold reduction in potency on the high affinity IL-2 receptor (hIL-2Rαβγ).

Embodiment 9. The modified hIL-2 protein of any one of the previous embodiments, wherein the modified hIL-2 protein exhibits about a 10,000-fold reduction in potency on the intermediate affinity IL-2 receptor (hIL-2Rβγ).

Embodiment 10. The modified hIL-2 protein of any one of embodiments 1 to 9, wherein the modified hIL-2 protein is fused to an anti-PD-1 antibody or an antigen-binding fragment thereof.

Embodiment 11. The modified hIL-2 protein of embodiment 10, wherein the modified hIL-2 protein is fused to the antibody or an antigen-binding fragment thereof at the N-terminus of an antibody light chain, the C-terminus of an antibody light chain, the N-terminus of an antibody heavy chain, the C-terminus of an antibody heavy chain, the N-terminus of the antigen-binding fragment, or the C-terminus of the antigen-binding fragment.

Embodiment 12. The modified hIL-2 protein of embodiment 10 or 11, wherein the modified hIL-2 protein is directly fused by a peptide bond to the antibody or an antigen-binding fragment thereof.

Embodiment 13. The modified hIL-2 protein of embodiment 12, wherein the modified hIL-2 is directly fused by a peptide bond to the C-terminal amino acid residue of the antibody heavy chain.

Embodiment 14. The modified hIL-2 protein of embodiment 10 or 11, wherein the modified hIL-2 protein is fused to the antibody or an antigen-binding fragment thereof through a linker.

Embodiment 15. A modified human interleukin-2 (hIL-2) protein, comprising a D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitution at amino acid position 20 and a R38E substitution at amino acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Embodiment 16. The modified hIL-2 protein of embodiment 15, comprising the amino acid sequence of any one of SEQ ID NOs: 307, 607-611, 614, 617, or 620.

Embodiment 17. The modified hIL-2 protein of embodiment 15 or 16, comprising a D20A substitution and a R38E substitution.

Embodiment 18. The modified hIL-2 protein of embodiment 17, comprising the amino acid sequence of SEQ ID NO: 149.

Embodiment 19. The modified hIL-2 protein of any one of embodiments 15-18, further comprising a deletion or substitution at amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Embodiment 20. The modified hIL-2 protein of embodiment 19, wherein the substitution at amino acid position 3 is T3A.

Embodiment 21. The modified hIL-2 protein of embodiment 20, comprising the amino acid sequence of SEQ ID NO: 216.

Embodiment 22. The modified hIL-2 protein of embodiment 19, comprising the amino acid sequence of SEQ ID NO: 218.

Embodiment 23. The modified hIL-2 protein of any one of embodiments 15-22, further comprising a deletion or substitution at amino acid position 125 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Embodiment 24. The modified hIL-2 protein of embodiment 23, wherein the substitution at amino acid position 125 is C125A.

Embodiment 25. The modified hIL-2 protein of embodiment 24, comprising the amino acid sequence of SEQ ID NO: 215, 217, or 219.

Embodiment 26. The modified hIL-2 protein of embodiment 25, comprising the amino acid sequence of SEQ ID NO: 217.

Embodiment 27. The modified hIL-2 protein of any one of embodiments 15 to 26, wherein the modified hIL-2 protein is fused to an anti-PD-1 antibody or an antigen-binding fragment thereof.

Embodiment 28. The modified hIL-2 protein of embodiment 27, wherein the modified hIL-2 protein is fused to the antibody or an antigen-binding fragment thereof at the N-terminus of an antibody light chain, the C-terminus of an antibody light chain, the N-terminus of an antibody heavy chain, the C-terminus of an antibody heavy chain, the N-terminus of the antigen-binding fragment, or the C-terminus of the antigen-binding fragment.

Embodiment 29. The modified hIL-2 protein of embodiment 27 or 28, wherein the modified hIL-2 protein is directly fused by a peptide bond to the antibody or an antigen-binding fragment thereof.

Embodiment 30. The modified hIL-2 protein of embodiment 29, wherein the modified hIL-2 is directly fused by a peptide bond to the C-terminal amino acid residue of the antibody heavy chain.

Embodiment 31. The modified hIL-2 protein of embodiment 27 or 28, wherein the modified hIL-2 protein is fused to the antibody or an antigen-binding fragment thereof through a linker.

Embodiment 32. A human antibody molecule, or antigen-binding fragment thereof, that immunospecifically binds to human programmed cell death protein-1 (hPD-1), wherein the human antibody molecule or antigen-binding fragment thereof comprises:

a) a heavy chain complementarity determining region 1 (CDR1) comprising the amino acid sequence of SEQ ID NO: 418, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 419, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 420, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 421, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 422, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 423;

b) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 386, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 387, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 388, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 389, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 390, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 391;

c) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 396, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 397, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 398, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 399, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 400, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 401; or

d) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 406, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 407, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 408, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 409, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 410, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 411.

Embodiment 33. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 32, comprising:

a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 416 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 417;

b) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 384 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 385;

c) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 394 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 395; or

d) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 404 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 405.

Embodiment 34. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 32 or 33, comprising a human IgG1 heavy chain constant region.

Embodiment 35. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 34, comprising an L235A substitution and a G237A substitution, according to EU numbering.

Embodiment 36. The human antibody molecule, or antigen-binding fragment thereof, of any one of embodiments 32-35, comprising:

a) a heavy chain comprising the amino acid sequence of SEQ ID NO: 414 and a light chain comprising the amino acid sequence of SEQ ID NO: 415;

b) a heavy chain comprising the amino acid sequence of SEQ ID NO: 424 and a light chain comprising the amino acid sequence of SEQ ID NO: 425;

c) a heavy chain comprising the amino acid sequence of SEQ ID NO: 426 and a light chain comprising the amino acid sequence of SEQ ID NO: 427; or

d) a heavy chain comprising the amino acid sequence of SEQ ID NO: 428 and a light chain comprising the amino acid sequence of SEQ ID NO: 429.

Embodiment 37. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 36, comprising a heavy chain comprising the amino acid sequence of SEQ ID NO: 414 and a light chain comprising the amino acid sequence of SEQ ID NO: 415.

Embodiment 38. The human antibody molecule, or antigen-binding fragment thereof, of any one of embodiments 32-37, fused to a modified human interleukin-2 (hIL-2) protein comprising a substitution at amino acid position 20 and a substitution at amino acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Embodiment 39. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 38, wherein the modified hIL-2 protein comprises the amino acid sequence of any one of SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620.

Embodiment 40. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 39, wherein the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 149.

Embodiment 41. The human antibody molecule, or antigen-binding fragment thereof, of any one of embodiments 38-40, wherein the modified hIL-2 protein further comprises a deletion or substitution at amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Embodiment 42. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 41, wherein the substitution at amino acid position 3 is T3A.

Embodiment 43. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 42, wherein the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 216.

Embodiment 44. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 41, wherein the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 218.

Embodiment 45. The human antibody molecule, or antigen-binding fragment thereof, of any one of embodiments 38-44, wherein the modified hIL-2 protein further comprises a deletion or substitution at amino acid position 125 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Embodiment 46. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 45, wherein the substitution at amino acid position 125 is C125A.

Embodiment 47. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 46, wherein the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 215, 217, or 219.

Embodiment 48. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 47, wherein the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 217.

Embodiment 49. The human antibody molecule, or antigen-binding fragment thereof, of any one of embodiments 38-48, wherein the modified hIL-2 protein is fused to the antibody or antigen-binding fragment thereof at the N-terminus of an antibody light chain, the C-terminus of an antibody light chain, the N-terminus of an antibody heavy chain, the C-terminus of an antibody heavy chain, the N-terminus of the antigen-binding fragment, or the C-terminus of the antigen-binding fragment.

Embodiment 50. The human antibody molecule, or antigen-binding fragment thereof, of any one of embodiments 38-49, wherein the modified hIL-2 protein is directly fused by a peptide bond to the antibody or antigen-binding fragment thereof.

Embodiment 51. The human antibody molecule, or antigen-binding fragment thereof, of embodiment 50, wherein the modified hIL-2 protein is directly fused by a peptide bond to the C-terminal amino acid residue of the antibody heavy chain.

Embodiment 52. The human antibody molecule, or antigen-binding fragment thereof, of any one of embodiments 38-49, wherein the modified hIL-2 protein is fused to the antibody or antigen-binding fragment through a linker.

Embodiment 53. An immunoconjugate comprising:

(a) a modified human interleukin-2 (hIL-2) protein comprising a substitution at amino acid position 20 and a substitution at amino acid position 38 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345; and

(b) a human antibody molecule, or antigen-binding fragment thereof, that immunospecifically binds to human programmed cell death protein-1 (hPD-1), wherein the human antibody molecule or antigen-binding fragment thereof comprises:

(i) a heavy chain complementarity determining region 1 (CDR1) comprising the amino acid sequence of SEQ ID NO: 418, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 419, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 420, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 421, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 422, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 423;

(ii) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 386, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 387, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 388, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 389, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 390, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 391;

(iii) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 396, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 397, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 398, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 399, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 400, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 401; or

(iv) a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO: 406, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 407, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 408, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 409, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 410, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 411.

Embodiment 54. The immunoconjugate of embodiment 53, wherein the substitution at amino acid position 20 of the modified hIL-2 protein is selected from a D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitution.

Embodiment 55. The immunoconjugate of embodiment 53 or 54, wherein the substitution at amino acid position 38 of the modified hIL-2 protein is selected from an R38E, R38N, R38G, R38H, R38I, R38L, R38M, R38F, R38P, R38S, R38T, R38W, R38Y, R38V, R38A, R38Q, R38D, and R38K substitution.

Embodiment 56. The immunoconjugate of any one of embodiments 53-55, wherein the substitution at amino acid position 20 of the modified hIL-2 protein is selected from a D20A, D20S, D20Q, D20M, D20I, D20V, D20N, D20G, D20T, or D20E substitution and the amino acid substitution at amino acid position 38 of the modified hIL-2 protein is R38E.

Embodiment 57. The immunoconjugate of any one of embodiments 53-56, wherein the modified hIL-2 protein comprises the amino acid sequence of any one of SEQ ID NOs: 134-150, 307, 344, 607-611, 614, 617, or 620.

Embodiment 58. The immunoconjugate of any one of embodiments 53-56, wherein the modified hIL-2 protein comprises a D20A and a R38E substitution.

Embodiment 59. The immunoconjugate of embodiment 58, wherein the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 149.

Embodiment 60. The immunoconjugate of any one of embodiments 53-57, comprising the amino acid sequence of any one of SEQ ID NOs: 608, 614, 611, 620, 607, 610, 617, 609, or 307.

Embodiment 61. The immunoconjugate of any one of embodiments 53-60, wherein the modified hIL-2 protein further comprises a deletion or substitution at amino acid position 3 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Embodiment 62. The immunoconjugate of embodiment 61, wherein the substitution at amino acid position 3 of the modified hIL-2 protein is T3A.

Embodiment 63. The immunoconjugate of embodiment 62, wherein the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 216.

Embodiment 64. The immunoconjugate of embodiment 61, wherein the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 218.

Embodiment 65. The immunoconjugate of any one of embodiments 53-64, wherein the modified hIL-2 protein further comprises a deletion or substitution at amino acid position 125 relative to the non-modified hIL-2 amino acid sequence of SEQ ID NO: 345.

Embodiment 66. The immunoconjugate of embodiment 65, wherein the substitution at amino acid position 125 is C125A.

Embodiment 67. The immunoconjugate of embodiment 66, wherein the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 215, 217, or 219.

Embodiment 68. The immunoconjugate of embodiment 67, wherein the modified hIL-2 protein comprises the amino acid sequence of SEQ ID NO: 217.

Embodiment 69. The immunoconjugate of any one of embodiments 53-68, wherein the modified hIL-2 protein is fused to the antibody or antigen-binding fragment thereof at the N-terminus of an antibody light chain, the C-terminus of an antibody light chain, the N-terminus of an antibody heavy chain, the C-terminus of an antibody heavy chain, the N-terminus of the antigen-binding fragment, or the C-terminus of the antigen-binding fragment.

Embodiment 70. The immunoconjugate of any one of embodiments 53-69, wherein the modified hIL-2 protein is directly fused by a peptide bond to the antibody or antigen-binding fragment thereof.

Embodiment 71. The immunoconjugate of embodiment 70, wherein modified hIL-2 protein is directly fused by a peptide bond to the C-terminal amino acid residue of the antibody heavy chain.

Embodiment 72. The immunoconjugate of any one of embodiments 53-69, wherein the modified hIL-2 protein is fused to the antibody or antigen-binding fragment thereof through a linker.

Embodiment 73. The immunoconjugate of any one of embodiments 53-72, wherein the human antibody molecule, or antigen-binding fragment thereof, comprises:

a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 416 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 417;

b) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 384 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 385;

c) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 394 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 395; or

d) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 404 and a light chain variable region comprising the amino acid sequence of SEQ ID NO: 405.

Embodiment 74. The immunoconjugate of any one of embodiments 53-73, wherein the human antibody molecule, or antigen-binding fragment thereof, comprises an IgG1 heavy chain constant region.

Embodiment 75. The immunoconjugate of embodiment 74, wherein the human antibody molecule, or antigen-binding fragment thereof, comprises an L235A substitution and a G237A substitution, according to EU numbering.

Embodiment 76. The immunoconjugate of any one of embodiments 53-75, wherein the human antibody molecule, or antigen-binding fragment thereof, comprises:

a) a heavy chain comprising the amino acid sequence of SEQ ID NO: 414 and a light chain comprising the amino acid sequence of SEQ ID NO: 415;

b) a heavy chain comprising the amino acid sequence of SEQ ID NO: 424 and a light chain comprising the amino acid sequence of SEQ ID NO: 425;

c) a heavy chain comprising the amino acid sequence of SEQ ID NO: 426 and a light chain comprising the amino acid sequence of SEQ ID NO: 427; or

d) a heavy chain comprising the amino acid sequence of SEQ ID NO: 428 and a light chain comprising the amino acid sequence of SEQ ID NO: 429.

Embodiment 77. The immunoconjugate of embodiment 76, wherein the human antibody molecule, or antigen-binding fragment thereof, comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 414 and a light chain comprising the amino acid sequence of SEQ ID NO: 415.

Embodiment 78. The immunoconjugate of any one of embodiments 53-77, comprising a light chain comprising the amino acid sequence of SEQ ID NO: 415; and a heavy chain-modified hIL-2 protein fusion comprising the amino acid sequence of SEQ ID NO: 532.

Embodiment 79. A pharmaceutical composition comprising the modified hIL-2 protein of any one of embodiments 1-31, the human antibody molecule, or antigen-binding fragment thereof, of any one of embodiments 32-52, or the immunoconjugate of any one of embodiments 53-78.

Embodiment 80. A polynucleotide, comprising a nucleic acid sequence encoding the modified hIL-2 protein of any one of embodiments 1-31, the human antibody molecule, or antigen-binding fragment thereof, of any one of embodiments 32-52, or the immunoconjugate of any one of embodiments 53-78.

Embodiment 81. A vector comprising a polynucleotide comprising a nucleic acid sequence that encodes the modified hIL-2 protein of any one of embodiments 1-31, the human antibody molecule, or antigen-binding fragment thereof, of any one of embodiments 32-52, or the immunoconjugate of any one of embodiments 53-78.

Embodiment 82. A transformed cell comprising the vector of embodiment 81.

Embodiment 83. A method of treating a disease or disorder in a subject, the method comprising administering a

therapeutically effective amount of the modified hIL-2 protein of any one of embodiments 10-14 and 27-31, the immunoconjugate of any one of embodiments 53-78, or the pharmaceutical composition of embodiment 79 to the subject to thereby treat the disease or disorder.

Embodiment 84. The method of embodiment 83, wherein the disease or disorder is cancer.

Embodiment 85. The method of embodiment 84, wherein the cancer is melanoma.

Embodiment 86. The method of embodiment 84, wherein the cancer is non-small cell lung carcinoma.

Embodiment 87. Use of the modified hIL-2 protein of any one of embodiments 10-14 and 27-31, the immunoconjugate of any one of embodiments 53-78, or the pharmaceutical composition of embodiment 79 in the preparation of a medicament for the treatment of a disease or disorder.

Embodiment 88. The use of embodiment 87, wherein the disease or disorder is cancer.

Embodiment 89. The use of embodiment 88, wherein the cancer is melanoma.

Embodiment 90. The use of embodiment 88, wherein the cancer is non-small cell lung carcinoma.

Embodiment 91. Use of the modified hIL-2 protein of any one of embodiments 10-14 and 27-31, the immunoconjugate of any one of embodiments 53-78, or the pharmaceutical composition of embodiment 79 for the treatment of a disease or disorder.

Embodiment 92. The use of embodiment 91, wherein the disease or disorder is cancer.

Embodiment 93. The use of embodiment 92, wherein the cancer is melanoma.

Embodiment 94. The use of embodiment 92, wherein the cancer is non-small cell lung carcinoma.

SEQUENCE LISTING

Sequence total quantity: 621

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mol_type = protein
organism = Synthetic construct
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WITFCQSIIS TLT 133

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organism = Synthetic construct
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WITFCQSIIS TLT 133

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WITFCQSIIS TLT 133

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WITFCQSIIS TLT 133

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mol_type = protein
organism = Synthetic construct

-continued

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WITFCQSIIS TLT                                                     133

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WITFCQSIIS TLT                                                     133

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WITFCQSIIS TLT                                                     133

SEQ ID NO: 11          moltype = AA  length = 133
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                       organism = Synthetic construct
SEQUENCE: 11
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEQL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 12          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 12
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEESL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 13          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 13
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEETL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 14          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
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                    organism = Synthetic construct
SEQUENCE: 14
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEWL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 15          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 15
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEYL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 16          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 16
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKKYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 17          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 17
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKKRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 18          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 18
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKFYMPKKA TELKHLQCLE  60
EELKPLEERL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 19          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 19
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFRMPKKA TELKHLQCLE  60
EELKPLEERL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 20          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 20
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKKRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 21          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 21
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTAML TKKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 22          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
```

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```
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 22
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TKKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 23          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 23
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKEFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 24          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 24
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKTFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 25          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 25
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKFRMPKKA TELKHLQCLE  60
EALKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 26          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 26
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKFRMPKKA TELKHLQCLE  60
EELKRLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 27          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 27
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKFRMPKKA TELKHLQCLE  60
EELKSLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 28          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 28
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKFRMPKKA TELKHLQCLE  60
EELKPLEEAL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 29          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 29
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKFRMPKKA TELKHLQCLE  60
EELKPLEEDL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 30          moltype = AA  length = 133
FEATURE                Location/Qualifiers
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```
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 30
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKFRMPKKA TELKHLQCLE  60
EELKPLEERL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 31           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 31
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 32           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 32
APTSSSTKKT QLQLEHLLLN LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 33           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 33
APTSSSTKKT QLQLEHLLLK LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 34           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 34
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISAIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 35           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 35
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISGIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 36           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 36
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISHIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 37           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 37
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISKIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 38           moltype = AA  length = 133
```

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```
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 38
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRALISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 39           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 39
APTSSSTKKT QLQLAHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 40           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 40
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 41           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 41
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISAIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 42           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 42
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLIANIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 43           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 43
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRALISAIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 44           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 44
APTSSSTKKT QLQLAHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISAIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 45           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 45
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLIAAIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133
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SEQ ID NO: 46          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 46
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTAML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 47          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 47
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTDML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 48          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 48
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 49          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 49
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTQML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 50          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 50
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TRKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 51          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 51
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TAKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 52          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 52
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TDKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 53          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 53
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML THKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133
```

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SEQ ID NO: 54          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 54
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFAFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 55          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 55
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFEFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 56          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 56
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFQFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 57          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 57
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFAMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 58          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 58
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFKMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 59          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 59
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFSMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 60          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 60
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 61          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 61
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
AELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
```

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WITFCQSIIS TLT                                                    133

SEQ ID NO: 62          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 62
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
RELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 63          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 63
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
KELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 64          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 64
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EALKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 65          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 65
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
ERLKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 66          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 66
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EKLKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 67          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 67
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EYLKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 68          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 68
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEYVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 69          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 69
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
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EELKPLEAVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 70          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 70
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEKVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 71          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 71
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLERVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 72          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 72
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLELVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 73          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 73
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NYAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 74          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 74
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NRAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 75          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 75
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NAAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 76          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 76
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NDAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 77          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 77
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APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NHAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 78          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 78
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NFAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 79          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 79
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTDML TFKFYMPKKA TELKHLQCLE  60
RELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 80          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 80
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTDML TFEFYMPKKA TELKHLQCLE  60
RELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 81          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 81
APASSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TAKFAMPKKA TELKHLQCLE  60
EELKPLEEVL NGAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFAQSIIS TLT                                                    133

SEQ ID NO: 82          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 82
APTSSSTKKT QLQLAHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 83          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 83
APTSSSTKKT QLQLRHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 84          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 84
APTSSSTKKT QLQLKHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 85          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
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SEQUENCE: 85
APTSSSTKKT QLQLEALLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 86          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 86
APTSSSTKKT QLQLEYLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 87          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 87
APTSSSTKKT QLQLEELLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 88          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 88
APTSSSTKKT QLQLEHLLAD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 89          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 89
APTSSSTKKT QLQLEHLLLI LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 90          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 90
APTSSSTKKT QLQLEHLLLS LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 91          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 91
APTSSSTKKT QLQLEHLLLH LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 92          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 92
APTSSSTKKT QLQLEHLLLT LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 93          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
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                    organism = Synthetic construct
SEQUENCE: 93
APTSSSTKKT QLQLEHLLLW LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 94          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 94
APTSSSTKKT QLQLEHLLLY LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 95          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 95
APTSSSTKKT QLQLEHLLLR LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 96          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 96
APTSSSTKKT QLQLEHLLLF LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 97          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 97
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL APRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 98          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 98
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRALISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 99          moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 99
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRRLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 100         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 100
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRKLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 101         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
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                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 101
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLIANIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 102         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 102
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISYIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 103         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 103
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISDIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 104         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 104
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISRIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 105         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 105
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISEIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 106         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 106
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISFIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 107         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 107
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISIIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 108         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 108
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VAVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 109         moltype = AA  length = 133
FEATURE                Location/Qualifiers
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```
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 109
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VYVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 110          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 110
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VSVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 111          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 111
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VFVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 112          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 112
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VRVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 113          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 113
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 114          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 114
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VEVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 115          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 115
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 116          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 116
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLRLKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 117          moltype = AA  length = 133
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FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 117
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLKLKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 118        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 118
APTSSSTKKT QLQLEELLLY LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 119        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 119
APTSSSTKKT QLQLEALLLY LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 120        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 120
APTSSSTKKT QLQLEYLLLY LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 121        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 121
APTSSSTKKT QLQLEHLLLY LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VAVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 122        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 122
APTSSSTKKT QLQLEHLLLY LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VSVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 123        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 123
APTSSSTKKT QLQLEHLLLY LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VRVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 124        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 124
APTSSSTKKT QLQLEHLLLY LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLRLKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133
```

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SEQ ID NO: 125          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 125
APTSSSTKKT QLQLEHLLLY LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 126          moltype = AA  length = 164
FEATURE                 Location/Qualifiers
source                  1..164
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 126
ELCDDDPPEI PHATFKAMAY KEGTMLNCEC KRGFRRIKSG SLYMLCTGNS SHSSWDNQCQ  60
CTSSATRNTT KQVTPQPEEQ KERKTTEMQS PMQPVDQASL PGHCREPPPW ENEATERIYH  120
FVVGQMVYYQ CVQGYRALHR GPAESVCKMT HGKTRWTQPQ LICT                   164

SEQ ID NO: 127          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 127
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TDKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 128          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 128
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TRKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 129          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 129
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TKKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 130          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 130
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TAKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 131          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 131
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML THKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 132          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 132
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133
```

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```
SEQ ID NO: 133          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 133
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFKMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 134          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 134
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTNML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 135          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 135
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTGML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 136          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 136
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTHML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 137          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 137
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTIML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 138          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 138
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTLML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 139          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 139
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTMML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 140          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 140
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTFML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
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WITFCQSIIS TLT                                                    133

SEQ ID NO: 141         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 141
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTPML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 142         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 142
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTSML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 143         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 143
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTTML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 144         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 144
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTWML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 145         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 145
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTYML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 146         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 146
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTVML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 147         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 147
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTAML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 148         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 148
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTQML TFKFYMPKKA TELKHLQCLE  60
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EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 149         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 149
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 150         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 150
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTDML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 151         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 151
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFEFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 152         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 152
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
AELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 153         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 153
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EALKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 154         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 154
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EYLKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 155         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 155
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NDAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 156         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 156
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APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NHAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 157         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 157
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NRAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 158         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 158
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TDKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 159         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 159
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TRKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 160         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 160
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML THKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 161         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 161
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TAKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 162         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 162
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFEFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 163         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 163
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 164         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
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SEQUENCE: 164
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFKMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 165         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 165
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EALKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 166         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 166
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EYLKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 167         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 167
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NDAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 168         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 168
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NHAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 169         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 169
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NRAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 170         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 170
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTDML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 171         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 171
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 172         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
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                    organism = Synthetic construct
SEQUENCE: 172
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTQML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 173         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 173
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTAML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 174         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 174
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISRIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 175         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 175
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRRLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 176         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 176
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRKLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 177         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 177
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TAKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 178         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 178
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML THKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 179         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 179
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTDML TFKFYMPKKA TELKHLQCLE  60
RELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 180         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
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                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 180
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
RELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 181         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 181
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTQML TFKFYMPKKA TELKHLQCLE  60
RELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 182         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 182
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTAML TFKFYMPKKA TELKHLQCLE  60
RELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 183         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 183
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTAML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 184         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 184
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTDML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 185         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 185
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 186         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 186
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTQML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 187         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 187
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TRKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 188         moltype = AA  length = 133
FEATURE                Location/Qualifiers
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source 1..133
mol_type = protein
organism = Synthetic construct

SEQUENCE: 188
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TAKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 189 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct

SEQUENCE: 189
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TDKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 190 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct

SEQUENCE: 190
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML THKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 191 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct

SEQUENCE: 191
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TKKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 192 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct

SEQUENCE: 192
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFAFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 193 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct

SEQUENCE: 193
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFEFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 194 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct

SEQUENCE: 194
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFQFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 195 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct

SEQUENCE: 195
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFAMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 196 moltype = AA length = 133

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FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 196
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFKMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 197        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 197
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFSMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 198        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 198
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 199        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 199
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
AELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 200        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 200
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EALKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 201        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 201
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
ERLKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 202        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 202
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EKLKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 203        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 203
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EYLKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133
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SEQ ID NO: 204 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct
SEQUENCE: 204
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE 60
EELKPLEYVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 205 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct
SEQUENCE: 205
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE 60
EELKPLEAVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 206 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct
SEQUENCE: 206
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE 60
EELKPLELVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 207 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct
SEQUENCE: 207
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NYAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 208 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct
SEQUENCE: 208
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NRAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 209 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct
SEQUENCE: 209
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NAAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 210 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct
SEQUENCE: 210
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NDAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 211 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct
SEQUENCE: 211
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NHAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

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SEQ ID NO: 212          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 212
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NFAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 213          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 213
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TKKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLIANIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 214          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 214
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TKKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 215          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 215
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFAQSIIS TLT                                                     133

SEQ ID NO: 216          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 216
APASSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 217          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 217
APASSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFAQSIIS TLT                                                     133

SEQ ID NO: 218          moltype = AA  length = 130
FEATURE                 Location/Qualifiers
source                  1..130
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 218
SSSTKKTQLQ LEHLLLALQM ILNGINNYKN PKLTEMLTFK FYMPKKATEL KHLQCLEEEL  60
KPLEEVLNLA QSKNFHLRPR DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT  120
FCQSIISTLT                                                         130

SEQ ID NO: 219          moltype = AA  length = 130
FEATURE                 Location/Qualifiers
source                  1..130
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 219
SSSTKKTQLQ LEHLLLALQM ILNGINNYKN PKLTEMLTFK FYMPKKATEL KHLQCLEEEL  60
KPLEEVLNLA QSKNFHLRPR DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT  120
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FAQSIISTLT                                                    130

SEQ ID NO: 220         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 220
APTSSSTKKT QLQLEHLLLD LAMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                 133

SEQ ID NO: 221         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 221
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WIAFCQSIIS TLT                                                 133

SEQ ID NO: 222         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 222
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIAS TLT                                                 133

SEQ ID NO: 223         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 223
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIA TLT                                                 133

SEQ ID NO: 224         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 224
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCASIIS TLT                                                 133

SEQ ID NO: 225         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 225
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCDSIIS TLT                                                 133

SEQ ID NO: 226         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 226
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCVSIIS TLT                                                 133

SEQ ID NO: 227         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 227
APTSSSTKKT QLQLEHLLLD LAMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
```

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EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIA TLT                                                     133

SEQ ID NO: 228         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 228
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKFRMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCDSIIS TLT                                                     133

SEQ ID NO: 229         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 229
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLALKGSE TTFMCEYADE TATIVEFLNR  120
WITFCDSIIS TLT                                                     133

SEQ ID NO: 230         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 230
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
RELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 231         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 231
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
NELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 232         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 232
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
DELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 233         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 233
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
QELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 234         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 234
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
GELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 235         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 235
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APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
HELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 236         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 236
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
IELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 237         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 237
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
LELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 238         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 238
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
KELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 239         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 239
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
MELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 240         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 240
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
FELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 241         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 241
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
PELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 242         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 242
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
SELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 243         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
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SEQUENCE: 243
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
TELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 244         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 244
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
WELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 245         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 245
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
YELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 246         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 246
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
VELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 247         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 247
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TNKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 248         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 248
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TQKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 249         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 249
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TEKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 250         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 250
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TGKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 251         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
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                     organism = Synthetic construct
SEQUENCE: 251
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TIKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 252         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 252
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TLKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 253         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 253
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TMKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 254         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 254
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TPKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 255         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 255
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TSKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 256         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 256
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TTKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 257         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 257
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TWKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 258         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 258
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TYKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 259         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
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```
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 259
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TVKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 260         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 260
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFAMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 261         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 261
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFNMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 262         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 262
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFDMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 263         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 263
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFQMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 264         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 264
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFEMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 265         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 265
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFGMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 266         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 266
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFHMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 267         moltype = AA  length = 133
FEATURE                Location/Qualifiers
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```
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 267
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFIMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 268          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 268
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFLMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 269          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 269
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFMMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 270          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 270
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFFMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 271          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 271
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFPMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 272          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 272
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFSMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 273          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 273
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFTMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 274          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 274
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFWMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 275          moltype = AA  length = 133
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```
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 275
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTRML TFKFVMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 276        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 276
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TNKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 277        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 277
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TQKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 278        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 278
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TEKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 279        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 279
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TGKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 280        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 280
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TIKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 281        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 281
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TLKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 282        moltype = AA  length = 133
FEATURE               Location/Qualifiers
source                1..133
                      mol_type = protein
                      organism = Synthetic construct
SEQUENCE: 282
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133
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SEQ ID NO: 283          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 283
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TMKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 284          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 284
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TPKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 285          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 285
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TSKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 286          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 286
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TTKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 287          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 287
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TWKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 288          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 288
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TYKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 289          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 289
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TVKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 290          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 290
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFAMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133
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SEQ ID NO: 291          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 291
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFNMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 292          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 292
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFDMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 293          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 293
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFQMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 294          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 294
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFEMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 295          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 295
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFGMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 296          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 296
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFHMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 297          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 297
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFIMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 298          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 298
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFLMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
```

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WITFCQSIIS TLT                                                    133

SEQ ID NO: 299         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 299
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFMMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 300         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 300
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFFMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 301         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 301
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFPMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 302         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 302
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFSMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 303         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 303
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFTMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 304         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 304
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFWMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 305         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 305
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFVMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VDVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 306         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 306
APTSSSTKKT QLQLEHLLLH LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
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EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 307         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 307
APTSSSTKKT QLQLEHLLLS LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 308         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 308
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TAKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISRIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 309         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 309
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TAKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISDIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 310         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 310
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRALISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 311         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 311
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRNLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 312         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 312
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRQLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 313         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 313
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRELISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 314         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 314
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APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRGLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 315         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 315
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRHLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 316         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 316
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRILISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 317         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 317
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRLLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 318         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 318
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRMLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 319         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 319
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRFLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 320         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 320
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRPLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 321         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 321
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRSLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 322         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
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SEQUENCE: 322
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRTLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 323         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 323
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRWLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 324         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 324
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRYLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 325         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 325
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRVLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 326         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 326
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VAVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 327         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 327
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VRVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 328         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 328
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VNVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 329         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 329
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VQVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 330         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
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                     organism = Synthetic construct
SEQUENCE: 330
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VEVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 331         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 331
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VGVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 332         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 332
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VHVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 333         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 333
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VLVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 334         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 334
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VKVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 335         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 335
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VMVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 336         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 336
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VFVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 337         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 337
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VPVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 338         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
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-continued

```
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 338
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VSVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 339         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 339
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VTVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 340         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 340
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VWVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 341         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 341
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VYVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 342         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 342
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VVVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 343         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 343
APTSSSTKKT QLQLEELLLD LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 344         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 344
APTSSSTKKT QLQLEHLLLA LQMILNGINN YKNPKLTKML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 345         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 345
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 346         moltype = AA  length = 268
FEATURE                Location/Qualifiers
```

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```
source                  1..268
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 346
PGWFLDSPDR PWNPPTFSPA LLVVTEGDNA TFTCSFSNTS ESFVLNWYRM SPSNQTDKLA  60
AFPEDRSQPG QDCRFRVTQL PNGRDFHMSV VRARRNDSGT YLCGAISLAP KAQIKESLRA  120
ELRVTERRAE VPTAHPSPSP RPAGQFQTLV VGVVGGLLGS LVLLVWVLAV ICSRAARGTI  180
GARRTGQPLK EDPSAVPVFS VDYGELDFQW REKTPEPPVP CVPEQTEYAT IVFPSGMGTS  240
SPARRGSADG PRSAQPLRPE DGHCSWPL                                      268

SEQ ID NO: 347          moltype = DNA  length = 804
FEATURE                 Location/Qualifiers
source                  1..804
                        mol_type = other DNA
                        organism = Synthetic construct
SEQUENCE: 347
ccaggatggt tcttagactc cccagacagg ccctggaacc cccccacctt ctccccagcc  60
ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg  120
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc  180
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg  240
cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc  300
tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca  360
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcaccc  420
aggccagccg gccagttcca aaccctggtg gttggtgtcg tgggcggcct gctgggcagc  480
ctggtgctgc tagtctgggt cctggccgtc atctgctccc gggccgcacg agggacaata  540
ggagccaggc gcaccggcca gcccctgaag gaggacccct cagccgtgcc tgtgttctct  600
gtggactatg gggagctgga tttccagtgg cgagagaaga ccccggagcc ccccgtgccc  660
tgtgtccctg agcagacgga gtatgccacc attgtctttc ctagcggaat gggcacctca  720
tcccccgccc gcaggggctc agctgacggc cctcggagtg cccagccact gaggcctgag  780
gatggacact gctcttggcc cctc                                          804

SEQ ID NO: 348          moltype = AA  length = 449
FEATURE                 Location/Qualifiers
source                  1..449
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 348
QVQLVESGGG VVQPGRSLRL DCKASGITFS NSGMHWVRQA PGKGLEWVAV IWYDGSKRYY  60
ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCATND DYWGQGTLVT VSSAKTTPPS  120
VYPLAPGCGD TTGSSVTLGC LVKGYFPESV TVTWNSGSLS SSVHTFPALL QSGLYTMSSS  180
VTVPSSTWPS QTVTCSVAHP ASSTTVDKKL EPSGPISTIN PCPPCKECHK CPAPNLEGGP  240
SVFIFPPNIK DVLMISLTPK VTCVVVDVSE DDPDVQISWF VNNVEVHTAQ TQTHREDYAS  300
TIRVVSTLPI QHQDWMSGKE FKCKVNNKDL PSPIERTISK IKGLVRAPQV YILPPPAEQL  360
SRKDVSLTCL VVGFNPGDIS VEWTSNGHTE ENYKDTAPVL DSDGSYFIYS KLNMKTSKWE  420
KTDSFSCNVR HEGLKNYYLK KTISRSPGK                                     449

SEQ ID NO: 349          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
source                  1..214
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 349
EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA  60
RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ SSNWPRTFGQ GTKVEIKRAD AAPTVSIFPP  120
SSEQLTSGGA SVVCFLNNFY PKDINVKWKI DGSERQNGVL NSWTDQDSKD STYSMSSTLT  180
LTKDEYERHN SYTCEATHKT STSPIVKSFN RNEC                               214

SEQ ID NO: 350          moltype = AA  length = 456
FEATURE                 Location/Qualifiers
source                  1..456
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 350
QVQLVQSGVE VKKPGASVKV SCKASGYTFT NYYMYWVRQA PGQGLEWMGG INPSNGGTNF  60
NEKFKNRVTL TTDSSTTTAY MELKSLQFDD TAVYYCARRD YRFDMGFDYW GQGTTVTVSS  120
AKTTPPSVYP LAPGCGDTTG SSVTLGCLVK GYFPESVTVT WNSGSLSSSV HTFPALLQSG  180
LYTMSSSVTV PSSTWPSQTV TCSVAHPASS TTVDKKLEPS GPISTINPCP PCKECHKCPA  240
PNLEGGPSVF IFPPNIKDVL MISLTPKVTC VVVDVSEDDP DVQISWFVNN VEVHTAQTQT  300
HREDYASTIR VVSTLPIQHQ DWMSGKEFKC KVNNKDLPSP IERTISKIKG LVRAPQVYIL  360
PPPAEQLSRK DVSLTCLVVG FNPGDISVEW TSNGHTEENY KDTAPVLDSD GSYFIYSKLN  420
MKTSKWEKTD SFSCNVRHEG LKNYYLKKTI SRSPGK                             456

SEQ ID NO: 351          moltype = AA  length = 218
FEATURE                 Location/Qualifiers
source                  1..218
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 351
EIVLTQSPAT LSLSPGERAT LSCRASKGVS TSGYSYLHWY QQKPGQAPRL LIYLASYLES  60
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GVPARFSGSG SGTDFTLTIS SLEPEDFAVY YCQHSRDLPL TFGGGTKVEI KRADAAPTVS  120
IFPPSSEQLT SGGASVVCFL NNFYPKDINV KWKIDGSERQ NGVLNSWTDQ DSKDSTYSMS  180
STLTLTKDEY ERHNSYTCEA THKTSTSPIV KSFNRNEC                         218

SEQ ID NO: 352         moltype = AA  length = 347
FEATURE                Location/Qualifiers
source                 1..347
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 352
LNTTILTPNG NEDTTADFFL TTMPTDSLSV STLPLPEVQC FVFNVEYMNC TWNSSSEPQP  60
TNLTLHYWYK NSDNDKVQKC SHYLFSEEIT SGCQLQKKEI HLYQTFVVQL QDPREPRRQA  120
TQMLKLQNLV IPWAPENLTL HKLSESQLEL NWNNRFLNHC LEHLVQYRTD WDHSWTEQSV  180
DYRHKFSLPS VDGQKRYTFR VRSRFNPLCG SAQHWSEWSH PIHWGSNTSK ENPFLFALEA  240
VVISVGSMGL IISLLCVYFW LERTMPRIPT LKNLEDLVTE YHGNFSAWSG VSKGLAESLQ  300
PDYSERLCLV SEIPPKGGAL GEGPGASPCN QHSPYWAPPC YTLKPET               347

SEQ ID NO: 353         moltype = AA  length = 525
FEATURE                Location/Qualifiers
source                 1..525
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 353
AVNGTSQFTC FYNSRANISC VWSQDGALQD TSCQVHAWPD RRRWNQTCEL LPVSQASWAC  60
NLILGAPDSQ KLTTVDIVTL RVLCREGVRW RVMAIQDFKP FENLRLMAPI SLQVVHVETH  120
RCNISWEISQ ASHYFERHLE FEARTLSPGH TWEEAPLLTL KQKQEWICLE TLTPDTQYEF  180
QVRVKPLQGE FTTWSPWSQP LAFRTKPAAL GKDTIPWLGH LLVGLSGAFG FIILVYLLIN  240
CRNTGPWLKK VLKCNTPDPS KFFSQLSSEH GGDVQKWLSS PFPSSSFSPG GLAPEISPLE  300
VLERDKVTQL LLQQDKVPEP ASLSSNHSLT SCFTNQGYFF FHLPDALEIE ACQVYFTYDP  360
YSEEDPDEGV AGAPTGSSPQ PLQPLSGEDD AYCTFPSRDD LLLFSPSLLG GPSPPSTAPG  420
GSGAGEERMP PSLQERVPRD WDPQPLGPPT PGVPDLVDFQ PPPELVLREA GEEVPDAGPR  480
EGVSFPWSRP PGQGEFRALN ARLPLNTDAY LSLQELQGQD PTHLV                  525

SEQ ID NO: 354         moltype = AA  length = 251
FEATURE                Location/Qualifiers
source                 1..251
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 354
ELCDDDPPEI PHATFKAMAY KEGTMLNCEC KRGFRRIKSG SLYMLCTGNS SHSSWDNQCQ  60
CTSSATRNTT KQVTPQPEEQ KERKTTEMQS PMQPVDQASL PGHCREPPPW ENEATERIYH  120
FVVGQMVYYQ CVQGYRALHR GPAESVCKMT HGKTRWTQPQ LICTGEMETS QFPGEEKPQA  180
SPEGRPESET SCLVTTTDFQ IQTEMAATME TSIFTTEYQV AVAGCVFLLI SVLLLSGLTW  240
QRRQRKSRRT I                                                       251

SEQ ID NO: 355         moltype = AA  length = 6
FEATURE                Location/Qualifiers
source                 1..6
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 355
SGGGGS                                                             6

SEQ ID NO: 356         moltype = AA  length = 346
FEATURE                Location/Qualifiers
source                 1..346
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 356
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLTDTVLTQS PALAVSPGER VTISCRASES VRTGVHWYQQ KPGQQPKLLI  180
YGASNLESGV PARFSGSGSG TDFTLTIDPV EADDTATYFC QQSWNDPFTF GSGTKLEIKR  240
TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS  300
KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC                 346

SEQ ID NO: 357         moltype = AA  length = 352
FEATURE                Location/Qualifiers
source                 1..352
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 357
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLTSGGGGSD TVLTQSPALA VSPGERVTIS CRASESVRTG VHWYQQKPGQ  180
QPKLLIYGAS NLESGVPARF SGSGSGTDFT LTIDPVEADD TATYFCQQSW NDPFTFGSGT  240
KLEIKRTVAA PSVFIFPPSD EQLKSGTASV VCLLNNFYPR EAKVQWKVDN ALQSGNSQES  300
VTEQDSKDST YSLSSTLTLS KADYEKHKVY ACEVTHQGLS SPVTKSFNRG EC          352
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SEQ ID NO: 358 moltype = AA length = 580
FEATURE Location/Qualifiers
source 1..580
mol_type = protein
organism = Synthetic construct
SEQUENCE: 358
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLTEVQLVES GGGLVQPGRS LKLSCAVSGF TFSDYAMAWV RQAPKKGLEW 180
VATISYDGSR TYYRDSVKGR FTISRDNAKI TLYLQMDSLR SEDTATYYCA RHGSGYFDYW 240
GQGVMVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV 300
HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP 360
PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA 420
KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ 480
VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY 540
SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 580

SEQ ID NO: 359 moltype = AA length = 586
FEATURE Location/Qualifiers
source 1..586
mol_type = protein
organism = Synthetic construct
SEQUENCE: 359
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLTSGGGGSE VQLVESGGGL VQPGRSLKLS CAVSGFTFSD YAMAWVRQAP 180
KKGLEWVATI SYDGSRTYYR DSVKGRFTIS RDNAKITLYL QMDSLRSEDT ATYYCARHGS 240
GYFDYWGQGV MVTVSSASTK GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP EPVTVSWNSG 300
ALTSGVHTFP AVLQSSGLYS LSSVVTVPSS SLGTQTYICN VNHKPSNTKV DKKVEPKSCD 360
KTHTCPPCPA PELLGGPSVF LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG 420
VEVHNAKTKP REEQYNSTYR VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG 480
QPREPQVYTL PPSRDELTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD 540
GSFFLYSKLT VDKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSPGK 586

SEQ ID NO: 360 moltype = AA length = 580
FEATURE Location/Qualifiers
source 1..580
mol_type = protein
organism = Synthetic construct
SEQUENCE: 360
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKAPT SSSTKKTQLQ LEHLLLDLQM ILNGINNYKN 480
PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR DLISNINVIV 540
LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 580

SEQ ID NO: 361 moltype = AA length = 586
FEATURE Location/Qualifiers
source 1..586
mol_type = protein
organism = Synthetic construct
SEQUENCE: 361
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSAPTSSST KKTQLQLEHL LLDLQMILNG 480
INNYKNPKLT RMLTFKFYMP KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS 540
NINVIVLELK GSETTFMCEY ADETATIVEF LNRWITFCQS IISTLT 586

SEQ ID NO: 362 moltype = AA length = 346
FEATURE Location/Qualifiers
source 1..346
mol_type = protein
organism = Synthetic construct
SEQUENCE: 362
DTVLTQSPAL AVSPGERVTI SCRASESVRT GVHWYQQKPG QQPKLLIYGA SNLESGVPAR 60
FSGSGSGTDF TLTIDPVEAD DTATYFCQQS WNDPFTFGSG TKLEIKRTVA APSVFIFPPS 120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL 180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GECAPTSSST KKTQLQLEHL LLDLQMILNG 240
INNYKNPKLT RMLTFKFYMP KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS 300

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NINVIVLELK GSETTFMCEY ADETATIVEF LNRWITFCQS IISTLT                346

SEQ ID NO: 363         moltype = AA  length = 352
FEATURE                Location/Qualifiers
source                 1..352
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 363
DTVLTQSPAL AVSPGERVTI SCRASESVRT GVHWYQQKPG QQPKLLIYGA SNLESGVPAR  60
FSGSGSGTDF TLTIDPVEAD DTATYFCQQS WNDPFTFGSG TKLEIKRTVA APSVFIFPPS  120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL  180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GECSGGGGSA PTSSSTKKTQ LQLEHLLLDL  240
QMILNGINNY KNPKLTRMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR  300
PRDLISNINV IVLELKGSET TFMCEYADET ATIVEFLNRW ITFCQSIIST LT          352

SEQ ID NO: 364         moltype = AA  length = 20
FEATURE                Location/Qualifiers
source                 1..20
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 364
SGGGGSGGGG SGGGGSGGGS                                             20

SEQ ID NO: 365         moltype = AA  length = 764
FEATURE                Location/Qualifiers
source                 1..764
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 365
ELCDDDPPEI PHATFKAMAY KEGTMLNCEC KRGFRRIKSG SLYMLCTGNS SHSSWDNQCQ  60
CTSSATRNTT KQVTPQPEEQ KERKTTEMQS PMQPVDQASL PGHCREPPPW ENEATERIYH  120
FVVGQMVYYQ CVQGYRALHR GPAESVCKMT HGKTRWTQPQ LICTSGGGGS GGGGSGGGGS  180
GGGSAPTSSS TKKTQLQLEH LLLDLQMILN GINNYKNPKL TRMLTFKFYM PKKATELKHL  240
QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL KGSETTFMCE YADETATIVE  300
FLNRWITFCQ SIISTLTEVQ LVESGGGLVQ PGRSLKLSCA VSGFTFSDYA MAWVRQAPKK  360
GLEWVATISY DGSRTYYRDS VKGRFTISRD NAKITLYLQM DSLRSEDTAT YYCARHGSGY  420
FDYWGQGVMV TVSSASTKGP SVFPLAPSSK STSGGTAALG CLVKDYFPEP VTVSWNSGAL  480
TSGVHTFPAV LQSSGLYSLS SVVTVPSSSL GTQTYICNVN HKPSNTKVDK KVEPKSCDKT  540
HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE  600
VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP  660
REPQVYTLPP SRDELTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS  720
FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK                  764

SEQ ID NO: 366         moltype = AA  length = 770
FEATURE                Location/Qualifiers
source                 1..770
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 366
ELCDDDPPEI PHATFKAMAY KEGTMLNCEC KRGFRRIKSG SLYMLCTGNS SHSSWDNQCQ  60
CTSSATRNTT KQVTPQPEEQ KERKTTEMQS PMQPVDQASL PGHCREPPPW ENEATERIYH  120
FVVGQMVYYQ CVQGYRALHR GPAESVCKMT HGKTRWTQPQ LICTSGGGGS GGGGSGGGGS  180
GGGSAPTSSS TKKTQLQLEH LLLDLQMILN GINNYKNPKL TRMLTFKFYM PKKATELKHL  240
QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL KGSETTFMCE YADETATIVE  300
FLNRWITFCQ SIISTLTSGG GGSEVQLVES GGGLVQPGRS LKLSCAVSGF TFSDYAMAWV  360
RQAPKKGLEW VATISYDGSR TYYRDSVKGR FTISRDNAKI TLYLQMDSLR SEDTATYYCA  420
RHGSGYFDYW GQGVMVTVSS ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS  480
WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP  540
KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW  600
YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS  660
KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV  720
LDSDGSFFLY SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK            770

SEQ ID NO: 367         moltype = AA  length = 530
FEATURE                Location/Qualifiers
source                 1..530
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 367
ELCDDDPPEI PHATFKAMAY KEGTMLNCEC KRGFRRIKSG SLYMLCTGNS SHSSWDNQCQ  60
CTSSATRNTT KQVTPQPEEQ KERKTTEMQS PMQPVDQASL PGHCREPPPW ENEATERIYH  120
FVVGQMVYYQ CVQGYRALHR GPAESVCKMT HGKTRWTQPQ LICTSGGGGS GGGGSGGGGS  180
GGGSAPTSSS TKKTQLQLEH LLLDLQMILN GINNYKNPKL TRMLTFKFYM PKKATELKHL  240
QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL KGSETTFMCE YADETATIVE  300
FLNRWITFCQ SIISTLTDTV LTQSPALAVS PGERVTISCR ASESVRTGVH WYQQKPGQQP  360
KLLIYGASNL ESGVPARFSG SGSGTDFTLT IDPVEADDTA TYFCQQSWND PFTFGSGTKL  420
EIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA KVQWKVDNAL QSGNSQESVT  480
EQDSKDSTYS LSSTLTLSKA DYEKHKVYAC EVTHQGLSSP VTKSFNRGEC            530
```

-continued

SEQ ID NO: 368 moltype = AA length = 536
FEATURE Location/Qualifiers
source 1..536
mol_type = protein
organism = Synthetic construct
SEQUENCE: 368
ELCDDDPPEI PHATFKAMAY KEGTMLNCEC KRGFRRIKSG SLYMLCTGNS SHSSWDNQCQ 60
CTSSATRNTT KQVTPQPEEQ KERKTTEMQS PMQPVDQASL PGHCREPPPW ENEATERIYH 120
FVVGQMVYYQ CVQGYRALHR GPAESVCKMT HGKTRWTQPQ LICTSGGGGS GGGGSGGGGS 180
GGGSAPTSSS TKKTQLQLEH LLLDLQMILN GINNYKNPKL TRMLTFKFYM PKKATELKHL 240
QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL KGSETTFMCE YADETATIVE 300
FLNRWITFCQ SIISTLTSGG GGSDTVLTQS PALAVSPGER VTISCRASES VRTGVHWYQQ 360
KPGQQPKLLI YGASNLESGV PARFSGSGSG TDFTLTIDPV EADDTATYFC QQSWNDPFTF 420
GSGTKLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN 480
SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC 536

SEQ ID NO: 369 moltype = AA length = 764
FEATURE Location/Qualifiers
source 1..764
mol_type = protein
organism = Synthetic construct
SEQUENCE: 369
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKELC DDDPPEIPHA TFKAMAYKEG TMLNCECKRG 480
FRRIKSGSLY MLCTGNSSHS SWDNQCQCTS SATRNTTKQV TPQPEEQKER KTTEMQSPMQ 540
PVDQASLPGH CREPPPWENE ATERIYHFVV GQMVYYQCVQ GYRALHRGPA ESVCKMTHGK 600
TRWTQPQLIC TSGGGGSGGG GSGGGGSGGG SAPTSSSTKK TQLQLEHLLL DLQMILNGIN 660
NYKNPKLTRM LTFKFYMPKK ATELKHLQCL EEELKPLEEV LNLAQSKNFH LRPRDLISNI 720
NVIVLELKGS ETTFMCEYAD ETATIVEFLN RWITFCQSII STLT 764

SEQ ID NO: 370 moltype = AA length = 770
FEATURE Location/Qualifiers
source 1..770
mol_type = protein
organism = Synthetic construct
SEQUENCE: 370
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 371 moltype = AA length = 530
FEATURE Location/Qualifiers
source 1..530
mol_type = protein
organism = Synthetic construct
SEQUENCE: 371
DTVLTQSPAL AVSPGERVTI SCRASESVRT GVHWYQQKPG QQPKLLIYGA SNLESGVPAR 60
FSGSGSGTDF TLTIDPVEAD DTATYFCQQS WNDPFTFGSG TKLEIKRTVA APSVFIFPPS 120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL 180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GECELCDDDP PEIPHATFKA MAYKEGTMLN 240
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 300
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 360
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM 420
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 480
DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 530

SEQ ID NO: 372 moltype = AA length = 536
FEATURE Location/Qualifiers
source 1..536
mol_type = protein
organism = Synthetic construct
SEQUENCE: 372
DTVLTQSPAL AVSPGERVTI SCRASESVRT GVHWYQQKPG QQPKLLIYGA SNLESGVPAR 60

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FSGSGSGTDF TLTIDPVEAD DTATYFCQQS WNDPFTFGSG TKLEIKRTVA APSVFIFPPS  120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL  180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GECSGGGGSE LCDDDPPEIP HATFKAMAYK  240
EGTMLNCECK RGFRRIKSGS LYMLCTGNSS HSSWDNQCQC TSSATRNTTK QVTPQPEEQK  300
ERKTTEMQSP MQPVDQASLP GHCREPPPWE NEATERIYHF VVGQMVYYQC VQGYRALHRG  360
PAESVCKMTH GKTRWTQPQL ICTSGGGGSG GGGSGGGGSG GGSAPTSSST KKTQLQLEHL  420
LLDLQMILNG INNYKNPKLT RMLTFKFYMP KKATELKHLQ CLEEELKPLE EVLNLAQSKN  480
FHLRPRDLIS NINVIVLELK GSETTFMCEY ADETATIVEF LNRWITFCQS IISTLT      536

SEQ ID NO: 373         moltype = AA  length = 448
FEATURE                Location/Qualifiers
source                 1..448
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 373
EVQLLESGGG LVQPGGSLRL SCAASGFTFK SYAMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLG                                     448

SEQ ID NO: 374         moltype = AA  length = 213
FEATURE                Location/Qualifiers
source                 1..213
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 374
DTVLTQSPAL AVSPGERVTI SCRASESVRT GVHWYQQKPG QQPKLLIYGA SNLESGVPAR  60
FSGSGSGTDF TLTIDPVEAD DTATYFCQQS WNDPFTFGSG TKLEIKRTVA APSVFIFPPS  120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL  180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC                               213

SEQ ID NO: 375         moltype = AA  length = 585
FEATURE                Location/Qualifiers
source                 1..585
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 375
EVQLQQSGPE LVKPGASVKI SCKTSGYTFT EYTMHWVKQS HGKSLEWIGG INPNNGGTTY  60
NQKFKGKATL TVDKSSSTAY MELRSLTSQD SAVYYCARDY YRYGHYYAMD YWGQGTSVTV  120
SSAKTTPPSV YPLAPGSAAQ TNSMVTLGCL VKGYFPEPVT VTWNSGSLSS GVHTFPAVLQ  180
SDLYTLSSSV TVPSSTWPSE TVTCNVAHPA SSTKVDKKIV PRDCGCKPCI CTVPEVSSVF  240
IFPPKPKDVL TITLTPKVTC VVVAISKDDP EVQFSWFVDD VEVHTAQTQP REEQFNSTFR  300
SVSELPIMHQ DWLNGKEFKC RVNSAAFPAP IEKTISKTKG RPKAPQVYTI PPPKEQMAKD  360
KVSLTCMITD FFPEDITVEW QWNGQPAENY KNTQPIMDTD GSYFVYSKLN VQKSNWEAGN  420
TFTCSVLHEG LHNHHTEKSL SHSPGKSGGG GSAPTSSSTK KTQLQLEHLL LDLQMILNGI  480
NNYKNPKLTR MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN  540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                  585

SEQ ID NO: 376         moltype = AA  length = 213
FEATURE                Location/Qualifiers
source                 1..213
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 376
QIVLTQSPAI MSASPGEKVT MTCSVSSSVR FMHWYQQKSG TSPKRWIYDT SKLASGVPAR  60
FSGSGSGTSY SLTISSMEAE DAATYYCQQW SSNPPTFGGG TKLKIKRADA APTVSIFPPS  120
SEQLTSGGAS VVCFLNNFYP KDINVKWKID GSERQNGVLN SWTDQDSKDS TYSMSSTLTL  180
TKDEYERHNS YTCEATHKTS TSPIVKSFNR NEC                               213

SEQ ID NO: 377         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 377
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCLSIIS TLT                                                     133

SEQ ID NO: 378         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 378
```

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APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCESIIS TLT                                                    133

SEQ ID NO: 379         moltype = AA  length = 447
FEATURE                Location/Qualifiers
source                 1..447
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 379
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGK                                     447

SEQ ID NO: 380         moltype = AA  length = 404
FEATURE                Location/Qualifiers
source                 1..404
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 380
MQIPQAPWPV VWAVLQLGWR PGWFLDSPDR PWNPPTFSPA LLVVTEGDNA TFTCSFSNTS  60
ESFVLNWYRM SPSNQTDKLA AFPEDRSQPG QDCRFRVTQL PNGRDFHMSV VRARRNDSGT  120
YLCGAISLAP KAQIKESLRA ELRVTERRAE VPTAHPSPSP RPAGQFQIEG RMDPKSCDKT  180
HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE  240
VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP  300
REPQVYTLPP SRDELTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS  360
FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK                  404

SEQ ID NO: 381         moltype = AA  length = 404
FEATURE                Location/Qualifiers
source                 1..404
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 381
MQIPQAPWPV VWAVLQLGWR PGWFLESPDR PWNAPTFSPA LLLVTEGDNA TFTCSFSNAS  60
ESFVLNWYRM SPSNQTDKLA AFPEDRSQPG QDCRFRVTRL PNGRDFHMSV VRARRNDSGT  120
YLCGAISLAP KAQIKESLRA ELRVTERRAE VPTAHPSPSP RPAGQFQIEG RMDPKSCDKT  180
HTCPPCPAPE LLGGPSVFLF PPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGVE  240
VHNAKTKPRE EQYNSTYRVV SVLTVLHQDW LNGKEYKCKV SNKALPAPIE KTISKAKGQP  300
REPQVYTLPP SRDELTKNQV SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS  360
FFLYSKLTVD KSRWQQGNVF SCSVMHEALH NHYTQKSLSL SPGK                  404

SEQ ID NO: 382         moltype = DNA  length = 367
FEATURE                Location/Qualifiers
source                 1..367
                       mol_type = other DNA
                       organism = Synthetic construct
SEQUENCE: 382
gaggtgcagc tgctggaaag cggcggcgga ctggtgcagc ctggaggcag cctgcggctg  60
tcttgtgccg cttctggctt caccttcaag gactactgca tgacctgggt cagacaggcc  120
cctggcaagg gcctcgagtg ggtgtccgcc atcgtgtaca gcggcgggtc aacatactac  180
gccgacagcg tgaagggcag attcacaatc agcagagata acagcaagaa caccctgtac  240
ctgcagatga acaacctgag agctgaagat accgccgtgt actactgcgc caagtacacc  300
agagccagct acttctacga cgccatggac gtgtggggcc agggcaccac cgtgacagtg  360
tcctcat                                                           367

SEQ ID NO: 383         moltype = DNA  length = 327
FEATURE                Location/Qualifiers
source                 1..327
                       mol_type = other DNA
                       organism = Synthetic construct
SEQUENCE: 383
gagatcgtgc tgacccagtc tcctggcacc ctgagcctga gccctggcga gagagctaca  60
ctgtcatgca gagcctctca gagcatcggc aagagcttcc tggcctggta ccagcaaaag  120
cctggacagg cccctagact gctgatctac gacgccagca ccagagccgc tgatatcccc  180
gccagattca gcggatctgg cagcggcact gatttcaccc tcaccatcag cagcctggaa  240
cccgaggact tcgccgtgta ctactgccag cagtactacg actggccccc cctgtctttt  300
ggcggaggca caaaggtgga aatcaag                                      327

SEQ ID NO: 384         moltype = AA  length = 122
FEATURE                Location/Qualifiers
source                 1..122
                       mol_type = protein
                       organism = Synthetic construct
```

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SEQUENCE: 384
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SS                                                                 122

SEQ ID NO: 385         moltype = AA  length = 109
FEATURE                Location/Qualifiers
source                 1..109
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 385
EIVLTQSPGT LSLSPGERAT LSCRASQSIG KSFLAWYQQK PGQAPRLLIY DASTRAADIP  60
ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ QYYDWPPLSF GGGTKVEIK              109

SEQ ID NO: 386         moltype = AA  length = 10
FEATURE                Location/Qualifiers
source                 1..10
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 386
GFTFKDYCMT                                                         10

SEQ ID NO: 387         moltype = AA  length = 17
FEATURE                Location/Qualifiers
source                 1..17
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 387
AIVYSGGSTY YADSVKG                                                 17

SEQ ID NO: 388         moltype = AA  length = 13
FEATURE                Location/Qualifiers
source                 1..13
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 388
YTRASYFYDA MDV                                                     13

SEQ ID NO: 389         moltype = AA  length = 12
FEATURE                Location/Qualifiers
source                 1..12
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 389
RASQSIGKSF LA                                                      12

SEQ ID NO: 390         moltype = AA  length = 7
FEATURE                Location/Qualifiers
source                 1..7
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 390
DASTRAA                                                            7

SEQ ID NO: 391         moltype = AA  length = 10
FEATURE                Location/Qualifiers
source                 1..10
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 391
QQYYDWPPLS                                                         10

SEQ ID NO: 392         moltype = DNA  length = 363
FEATURE                Location/Qualifiers
source                 1..363
                       mol_type = other DNA
                       organism = Synthetic construct
SEQUENCE: 392
caggttcagc tggttcagtc tggcagcgag ctgaagaaac ctggcgcctc tgtgaaggtg  60
tcctgcaagg cctctggcta cagcctgtac ggcacctcta tgcactgggt ccgacaggct  120
ccaggacagg gacttgagtg gatgggctac atcagcccct ttaccggcag agccacatac  180
gcccagggct tcacaggcag attcgtgttc agcctggaca ccagcgtgtc cacagcctac  240
ctgcagatca gctctctgaa ggccgaggac accgccgtgt actactgcgc cagagactac  300
gactaccggt actactatgc catggactac tggggccagg gcaccacagt tacagtgtcc  360
tca                                                                363

SEQ ID NO: 393         moltype = DNA  length = 324
FEATURE                Location/Qualifiers
source                 1..324
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```
                     mol_type = other DNA
                     organism = Synthetic construct
SEQUENCE: 393
gaaattgtgc tgacacagag ccccgacttc cagagcgtga cccctaaaga aaaagtgacc  60
atcacctgta ccgccagcga gtccgtgcct cctcagttcc tgcattggta tcagcagaag  120
cccgatcaga gccccaagct gctgatctac gccagcagag aaagagccag cggcgtccca  180
agcagatttt ctggctctgg cagcggcacc gacttcaccc tgacaatcaa tagcctggaa  240
gccgaggacg ccgccaccta ctactgccac cagtttcaca gaagccctct gacctttggc  300
ggaggcacca agctggaaat caag                                         324

SEQ ID NO: 394         moltype = AA  length = 121
FEATURE                Location/Qualifiers
source                 1..121
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 394
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY  60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS  120
S                                                                  121

SEQ ID NO: 395         moltype = AA  length = 108
FEATURE                Location/Qualifiers
source                 1..108
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 395
EIVLTQSPDF QSVTPKEKVT ITCTASESVP PQFLHWYQQK PDQSPKLLIY ASRERASGVP  60
SRFSGSGSGT DFTLTINSLE AEDAATYYCH QFHRSPLTFG GGTKLEIK               108

SEQ ID NO: 396         moltype = AA  length = 10
FEATURE                Location/Qualifiers
source                 1..10
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 396
GYSLYGTSMH                                                         10

SEQ ID NO: 397         moltype = AA  length = 17
FEATURE                Location/Qualifiers
source                 1..17
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 397
YISPFTGRAT YAQGFTG                                                 17

SEQ ID NO: 398         moltype = AA  length = 12
FEATURE                Location/Qualifiers
source                 1..12
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 398
DYDYRYYYAM DY                                                      12

SEQ ID NO: 399         moltype = AA  length = 12
FEATURE                Location/Qualifiers
source                 1..12
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 399
TASESVPPQF LH                                                      12

SEQ ID NO: 400         moltype = AA  length = 7
FEATURE                Location/Qualifiers
source                 1..7
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 400
ASRERAS                                                            7

SEQ ID NO: 401         moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 401
HQFHRSPLT                                                          9

SEQ ID NO: 402         moltype = DNA  length = 345
FEATURE                Location/Qualifiers
```

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```
source                  1..345
                        mol_type = other DNA
                        organism = Synthetic construct
SEQUENCE: 402
gacgtgcagc tggtggaaag cggcggaggc ctggtccagc ccggcggctc tctgagactg  60
agctgcgccg ccagcggctt caccttcgac atcagcgcca tgagctgggt gcggcaggcc  120
cctggcaagg gcctggaatg ggtcagcaca atcagcggat ctgcctacag cacctactac  180
gccgacagcg tgaagggcag attcaccatc tcaagagata acagcaagag caccctgtac  240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt actactgcgc cagagagatc  300
ttcagcgact actggggctt gggcaccctg gtgacagtgt cctca                  345

SEQ ID NO: 403          moltype = DNA  length = 330
FEATURE                 Location/Qualifiers
source                  1..330
                        mol_type = other DNA
                        organism = Synthetic construct
SEQUENCE: 403
caaagcgtgc tgacacagcc ccccagcgct tctggcaccc ctggccagag agtgaccatc  60
tcatgcagcg ggtcaacaag caacatcggc agagagagcg tgtactggta ccagcagctg  120
cctggaaccg cccctaagct gctgatctac agcaacgtgc agcggcctag cggcgccct   180
aacagattca gcggcagcaa gagcggcacc agcgccagcc tggccatcag cggcctgcag  240
agcgaggacg aggccgacta ctactgcggc acatgggacg acagcctgaa cggctgggtg  300
ttcggcggcg gaactaagct gaccgtccta                                   330

SEQ ID NO: 404          moltype = AA  length = 115
FEATURE                 Location/Qualifiers
source                  1..115
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 404
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSS       115

SEQ ID NO: 405          moltype = AA  length = 110
FEATURE                 Location/Qualifiers
source                  1..110
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 405
QSVLTQPPSA SGTPGQRVTI SCSGSTSNIG RESVYWYQQL PGTAPKLLIY SNVQRPSGAP  60
NRFSGSKSGT SASLAISGLQ SEDEADYYCG TWDDSLNGWV FGGGTKLTVL             110

SEQ ID NO: 406          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 406
GFTFDISAMS                                                         10

SEQ ID NO: 407          moltype = AA  length = 17
FEATURE                 Location/Qualifiers
source                  1..17
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 407
TISGSAYSTY YADSVKG                                                 17

SEQ ID NO: 408          moltype = AA  length = 6
FEATURE                 Location/Qualifiers
source                  1..6
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 408
EIFSDY                                                             6

SEQ ID NO: 409          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 409
SGSTSNIGRE SVY                                                     13

SEQ ID NO: 410          moltype = AA  length = 7
FEATURE                 Location/Qualifiers
source                  1..7
                        mol_type = protein
                        organism = Synthetic construct
```

-continued

SEQUENCE: 410
SNVQRPS 7

SEQ ID NO: 411 moltype = AA length = 11
FEATURE Location/Qualifiers
source 1..11
mol_type = protein
organism = Synthetic construct
SEQUENCE: 411
GTWDDSLNGW V 11

SEQ ID NO: 412 moltype = DNA length = 1755
FEATURE Location/Qualifiers
source 1..1755
mol_type = other DNA
organism = Synthetic construct
SEQUENCE: 412
gaggtgcagc tgctggaaag cggcggcggc ctcgtgcagc ctggcggatc tctgcggctg 60
agctgtgctg ccagcggctt cacatttaaa tcctacgcca tgcactgggt tagacaagcc 120
cccggaaagg gcctggaatg ggtgtccgcc atcgtctaca gcggcggatc tacatactac 180
gccgacagcg tgaagggccg gttcaccatc agcagagata atagcaagaa caccctgtac 240
ctgcagatga acagcctgag agccgaggac accgccgtgt actactgcgc caagtacgac 300
agagcttctt atttctacga tgccatggac gtgtggggcc agggcaccac cgtgacagtg 360
tcctcagcta gcaccaaggg ccctagcgtg tttccactgg cccctagctc taaaagcaca 420
agcggcggaa ccgccgctct gggttgtctg gtgaaggact acttccctga gcctgtgacc 480
gtcagctgga acagcggcgc cctgaccagc ggcgttcaca cattccccgc tgtgctgcag 540
agctctgggc tgtacagcct gagcagcgtg gtgaccgtgc cttcttcttc tctgggcaca 600
caaacataca tctgcaacgt gaaccacaag cccagtaata ccaaagtgga taagaaggtg 660
gaacctaagt cttgcgacaa gacccacacc tgtcctccgt gccctgctcc tgaactggct 720
ggagctccca gcgtgttcct gttcccccc aaacctaaag acaccctgat gatcagccgg 780
acccctgagg tgacctgcgt ggtcgtcgac gtgtcccacg aagatcctga ggtgaagttc 840
aactggtacg tggacggcgt ggaagtgcat aatgccaaga caaagcctag agaggaacag 900
tacaacagca cctatagagt ggtgtccgtg ctgacagtgc tgcaccagga ctggctgaac 960
ggcaaggaat acaagtgcaa ggtgtccaac aaggccctcc ccgcccctat cgagaagacc 1020
atcagcaagg caaagggcca acctagagag ccccaggtgt acaccctgcc tccaagcaga 1080
gatgagctga ccaagaacca ggttagcctg acttgtctgg tgaaaggctt ctacccctcc 1140
gatatcgccg tggaatggga gagcaacggc cagcctgaga acaactacaa gaccacacct 1200
ccagtgctgg acagcgacgg cagcttcttc ctgtatagca agctgacagt ggacaagagc 1260
agatggcagc agggcaacgt gttcagctgc agcgtcatgc acgaggccct gcacaaccac 1320
tacacccaga agtctctgag cctgagccct ggaaaggccc ctgcttctag cagcaccaag 1380
aagacccagc tgcagctgga acacctgctg ctggccctgc agatgatcct gaacggcatc 1440
aacaactaca agaaccccaa gctgaccgag atgctgacat ttaagttcta catgcctaag 1500
aaagccaccg agctgaagca cctgcaatgt ctggaagaag agctgaaacc tctggaagag 1560
gtgctgaatc tggctcagtc aaagaacttc caccttagac ctagagatct gatcagcaac 1620
atcaacgtga tcgtgctgga actgaagggc agcgagacga ccttcatgtg cgagtacgcc 1680
gacgagacag ccacaatcgt ggagttcctg aacagatgga tcaccttcgc ccagagcatc 1740
atctccaccc tgacc 1755

SEQ ID NO: 413 moltype = DNA length = 648
FEATURE Location/Qualifiers
source 1..648
mol_type = other DNA
organism = Synthetic construct
SEQUENCE: 413
gagatcgtgc tgacccagtc cccaggcaca ctgagcctga gccccggcga gcgggccacc 60
ctgagctgta gagctagcca gagcatctcc agcagcttcc tggcctggta ccagcagaaa 120
cctggccagg cccctagact gctgatctac gacgcctctg atagagctac aggcatcccc 180
gaccggttca gcggcagcgg atctggcacc gacttcaccc tgaccatcag cagactcgag 240
cctgaagatt tcgccgtgta ctactgccag caatactatg actggcctcc tctgtctttt 300
ggcggcggaa caaaggtgga aattaagcgt acggtggcgg cgcccagcgt gttcatcttc 360
ccacccagcg acgagcagct gaagtccggc acagccagcg tggtgtgcct gctgaacaac 420
ttctaccccc gcgaggccaa ggtgcagtgg aaggtggaca acgccctgca gagcggcaac 480
agccaggaaa gcgtgaccga gcaggacagc aaggactcca cctacagcct gagcagcacc 540
ctgaccctga gcaaggccga ctacgagaag cacaaggtgt acgcctgcga agtgacccac 600
cagggcctgt ccagccccgt gaccaagagc ttcaaccggg gcgagtgc 648

SEQ ID NO: 414 moltype = AA length = 451
FEATURE Location/Qualifiers
source 1..451
mol_type = protein
organism = Synthetic construct
SEQUENCE: 414
EVQLLESGGG LVQPGGSLRL SCAASGFTFK SYAMHWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYD RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA 240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420

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RWQQGNVFSC SVMHEALHNH YTQKSLSLSP G 451

SEQ ID NO: 415 moltype = AA length = 216
FEATURE Location/Qualifiers
source 1..216
mol_type = protein
organism = Synthetic construct
SEQUENCE: 415
EIVLTQSPGT LSLSPGERAT LSCRASQSIS SSFLAWYQQK PGQAPRLLIY DASDRATGIP 60
DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYYDWPPLSF GGGTKVEIKR TVAAPSVFIF 120
PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST 180
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC 216

SEQ ID NO: 416 moltype = AA length = 122
FEATURE Location/Qualifiers
source 1..122
mol_type = protein
organism = Synthetic construct
SEQUENCE: 416
EVQLLESGGG LVQPGGSLRL SCAASGFTFK SYAMHWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYD RASYFYDAMD VWGQGTTVTV 120
SS 122

SEQ ID NO: 417 moltype = AA length = 109
FEATURE Location/Qualifiers
source 1..109
mol_type = protein
organism = Synthetic construct
SEQUENCE: 417
EIVLTQSPGT LSLSPGERAT LSCRASQSIS SSFLAWYQQK PGQAPRLLIY DASDRATGIP 60
DRFSGSGSGT DFTLTISRLE PEDFAVYYCQ QYYDWPPLSF GGGTKVEIK 109

SEQ ID NO: 418 moltype = AA length = 10
FEATURE Location/Qualifiers
source 1..10
mol_type = protein
organism = Synthetic construct
SEQUENCE: 418
GFTFKSYAMH 10

SEQ ID NO: 419 moltype = AA length = 17
FEATURE Location/Qualifiers
source 1..17
mol_type = protein
organism = Synthetic construct
SEQUENCE: 419
AIVYSGGSTY YADSVKG 17

SEQ ID NO: 420 moltype = AA length = 13
FEATURE Location/Qualifiers
source 1..13
mol_type = protein
organism = Synthetic construct
SEQUENCE: 420
YDRASYFYDA MDV 13

SEQ ID NO: 421 moltype = AA length = 12
FEATURE Location/Qualifiers
source 1..12
mol_type = protein
organism = Synthetic construct
SEQUENCE: 421
RASQSISSSF LA 12

SEQ ID NO: 422 moltype = AA length = 7
FEATURE Location/Qualifiers
source 1..7
mol_type = protein
organism = Synthetic construct
SEQUENCE: 422
DASDRAT 7

SEQ ID NO: 423 moltype = AA length = 10
FEATURE Location/Qualifiers
source 1..10
mol_type = protein
organism = Synthetic construct
SEQUENCE: 423
QQYYDWPPLS 10

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SEQ ID NO: 424 moltype = AA length = 448
FEATURE Location/Qualifiers
source 1..448
mol_type = protein
organism = Synthetic construct
SEQUENCE: 424
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP 240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM 360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ 420
EGNVFSCSVM HEALHNHYTQ KSLSLSLG 448

SEQ ID NO: 425 moltype = AA length = 216
FEATURE Location/Qualifiers
source 1..216
mol_type = protein
organism = Synthetic construct
SEQUENCE: 425
EIVLTQSPGT LSLSPGERAT LSCRASQSIG KSFLAWYQQK PGQAPRLLIY DASTRAADIP 60
ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ QYYDWPPLSF GGGTKVEIKR TVAAPSVFIF 120
PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST 180
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC 216

SEQ ID NO: 426 moltype = AA length = 447
FEATURE Location/Qualifiers
source 1..447
mol_type = protein
organism = Synthetic construct
SEQUENCE: 426
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY 60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS 120
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS 180
SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFLGGPS 240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT 360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE 420
GNVFSCSVMH EALHNHYTQK SLSLSLG 447

SEQ ID NO: 427 moltype = AA length = 215
FEATURE Location/Qualifiers
source 1..215
mol_type = protein
organism = Synthetic construct
SEQUENCE: 427
EIVLTQSPDF QSVTPKEKVT ITCTASESVP PQFLHWYQQK PDQSPKLLIY ASRERASGVP 60
SRFSGSGSGT DFTLTINSLE AEDAATYYCH QFHRSPLTFG GGTKLEIKRT VAAPSVFIFP 120
PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL 180
TLSKADYEKH KVYACEVTHQ GLSSPVTKSF NRGEC 215

SEQ ID NO: 428 moltype = AA length = 441
FEATURE Location/Qualifiers
source 1..441
mol_type = protein
organism = Synthetic construct
SEQUENCE: 428
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY 60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG 120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL 180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP 240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL 360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC 420
SVMHEALHNH YTQKSLSLSL G 441

SEQ ID NO: 429 moltype = AA length = 216
FEATURE Location/Qualifiers
source 1..216
mol_type = protein
organism = Synthetic construct
SEQUENCE: 429
QSVLTQPPSA SGTPGQRVTI SCSGSTSNIG RESVYWYQQL PGTAPKLLIY SNVQRPSGAP 60
NRFSGSKSGT SASLAISGLQ SEDEADYYCG TWDDSLNGWV FGGGTKLTVL GQPKAAPSVT 120
LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS 180
YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS 216

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SEQ ID NO: 430 moltype = AA length = 582
FEATURE Location/Qualifiers
source 1..582
mol_type = protein
organism = Synthetic construct
SEQUENCE: 430
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP 240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM 360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ 420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PTSSSTKKTQ LQLEHLLLAL QMILNGINNY 480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV 540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFCQSIIST LT 582

SEQ ID NO: 431 moltype = AA length = 585
FEATURE Location/Qualifiers
source 1..585
mol_type = protein
organism = Synthetic construct
SEQUENCE: 431
EVQLLESGGG LVQPGGSLRL SCAASGFTFK SYAMHWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYD RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA 240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI 480
NNYKNPKLTR MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN 540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT 585

SEQ ID NO: 432 moltype = AA length = 587
FEATURE Location/Qualifiers
source 1..587
mol_type = protein
organism = Synthetic construct
SEQUENCE: 432
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY 60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS 120
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS 180
SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFLGGPS 240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST 300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT 360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE 420
GNVFSCSVMH EALHNHYTQK SLSLSLGKSG GGGSAPTSSS TKKTQLQLEH LLLALQMILN 480
GINNYKNPKL TEMLTFKFYM PKKATELKHL QCLEEELKPL EEVLNLAQSK NFHLRPRDLI 540
SNINVIVLEL KGSETTFMCE YADETATIVE FLNRWITFCQ SIISTLT 587

SEQ ID NO: 433 moltype = AA length = 575
FEATURE Location/Qualifiers
source 1..575
mol_type = protein
organism = Synthetic construct
SEQUENCE: 433
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY 60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG 120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL 180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP 240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL 360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC 420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTE 480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG 540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT 575

SEQ ID NO: 434 moltype = AA length = 577
FEATURE Location/Qualifiers
source 1..577
mol_type = protein
organism = Synthetic construct
SEQUENCE: 434
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF 240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300

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SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKAPTSSS TKKTQLQLEH LLLALQMILN GINNYKNPKL  480
TEMLTFKFYM PKKATELKHL QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL  540
KGSETTFMCE YADETATIVE FLNRWITFCQ SIISTLT                           577

SEQ ID NO: 435         moltype = AA  length = 582
FEATURE                Location/Qualifiers
source                 1..582
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 435
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLAL QMILNGINNY  480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV  540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT                     582

SEQ ID NO: 436         moltype = DNA  length = 441
FEATURE                Location/Qualifiers
source                 1..441
                       mol_type = other DNA
                       organism = Synthetic construct
SEQUENCE: 436
ccaggatggt tcttagactc cccagacagg ccctggaacc cccccacctt ctccccagcc  60
ctgctcgtgg tgaccgaagg ggacaacgcc accttcacct gcagcttctc caacacatcg  120
gagagcttcg tgctaaactg gtaccgcatg agccccagca accagacgga caagctggcc  180
gccttccccg aggaccgcag ccagcccggc caggactgcc gcttccgtgt cacacaactg  240
cccaacgggc gtgacttcca catgagcgtg gtcagggccc ggcgcaatga cagcggcacc  300
tacctctgtg gggccatctc cctggccccc aaggcgcaga tcaaagagag cctgcgggca  360
gagctcaggg tgacagagag aagggcagaa gtgcccacag cccaccccag cccctcaccc  420
aggccagccg gccagttcca a                                             441

SEQ ID NO: 437         moltype = AA  length = 147
FEATURE                Location/Qualifiers
source                 1..147
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 437
PGWFLDSPDR PWNPPTFSPA LLVVTEGDNA TFTCSFSNTS ESFVLNWYRM SPSNQTDKLA  60
AFPEDRSQPG QDCRFRVTQL PNGRDFHMSV VRARRNDSGT YLCGAISLAP KAQIKESLRA  120
ELRVTERRAE VPTAHPSPSP RPAGQFQ                                      147

SEQ ID NO: 438         moltype = AA  length = 448
FEATURE                Location/Qualifiers
source                 1..448
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 438
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SNYMSWVRQA PGKGLEWVSA ISSSGGTIFY  60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHK WNAVYYDGMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLG                                     448

SEQ ID NO: 439         moltype = AA  length = 216
FEATURE                Location/Qualifiers
source                 1..216
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 439
QSVLTQPPSA SGTPGQRVTI SCSGSNSNIG RNLVNWYQQL PGTAPKLLIY TIDQRPSGVP  60
DRFSGSKSGT SASLVISGLQ SEDEADYYCA AWDGSLNAWV FGGGTKLTVL GQPKAAPSVT  120
LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS  180
YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS                            216

SEQ ID NO: 440         moltype = AA  length = 445
FEATURE                Location/Qualifiers
source                 1..445
                       mol_type = protein
                       organism = Synthetic construct
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SEQUENCE: 440
EVQLLESGGG LVQPGGSLRL SCTASGFTFS SYEMQWVRQA PGKGLEWVLG ITSSSSHIFY 60
ADSVKGRFTV SRDNSKNTLY LQMNSLRAED TAVYYCTKDL NSYYGLDVWG QGTTVTVSSA 120
STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG 180
LYSLSSVVTV PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF 240
LFPPKPKDTL MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR 300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN 360
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT VDKSRWQEGN 420
VFSCSVMHEA LHNHYTQKSL SLSLG 445

SEQ ID NO: 441 moltype = AA length = 216
FEATURE Location/Qualifiers
source 1..216
mol_type = protein
organism = Synthetic construct
SEQUENCE: 441
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DRFSGSKSGT SASLAISGLQ SDDEADYYCS SWDASLNVWV FGGGTKLTVL GQPKAAPSVT 120
LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS 180
YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS 216

SEQ ID NO: 442 moltype = AA length = 448
FEATURE Location/Qualifiers
source 1..448
mol_type = protein
organism = Synthetic construct
SEQUENCE: 442
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYYMSWVRQA PGKGLEWVSA ISSSGGTIFY 60
ADSVKGRFII SRDNSKNTLY LQMNSLRAED TAVYYCAKHK WNDVYYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP 240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM 360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ 420
EGNVFSCSVM HEALHNHYTQ KSLSLSLG 448

SEQ ID NO: 443 moltype = AA length = 216
FEATURE Location/Qualifiers
source 1..216
mol_type = protein
organism = Synthetic construct
SEQUENCE: 443
QSVLTQPPSA SGTPGQRVTI SCSGSNSNIG RNLVNWYQQL PGTAPKLLIY TVDQRPSGVP 60
DRFSGSKSGT SASLAISGLA SEDEADYYCA AWDSSLNSWV FGGGTKLTVL GQPKAAPSVT 120
LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS 180
YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS 216

SEQ ID NO: 444 moltype = AA length = 441
FEATURE Location/Qualifiers
source 1..441
mol_type = protein
organism = Synthetic construct
SEQUENCE: 444
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY 60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG 120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL 180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP 240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL 360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC 420
SVMHEALHNH YTQKSLSLSL G 441

SEQ ID NO: 445 moltype = AA length = 216
FEATURE Location/Qualifiers
source 1..216
mol_type = protein
organism = Synthetic construct
SEQUENCE: 445
QSVLTQPPSA SGTPGQRVTI SCSGNTSNIG RESVYWYQQL PGTAPKLLIY SNVQRPSGVP 60
DRFSGSKSGT SASLAISGLQ SEDEADYYCG TWDDSLNGWV FGGGTKLTVL GQPKAAPSVT 120
LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS 180
YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS 216

SEQ ID NO: 446 moltype = AA length = 440
FEATURE Location/Qualifiers
source 1..440
mol_type = protein
organism = Synthetic construct
SEQUENCE: 446

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DSLVESGGGL VQPGGSLRLS CAASGFTFDI SAMSWVRQAP GKGLEWVSTI SGSAYSTYYA  60
DSVKGRFTIS RDNSKSTLYL QMNSLRAEDT AVYYCAREIF SDYWGLGTLV TVSSASTKGP  120
SVFPLAPCSR STSESTAALG CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS  180
SVVTVPSSSL GTKTYTCNVD HKPSNTKVDK RVESKYGPPC PPCPAPEFLG GPSVFLFPPK  240
PKDTLMISRT PEVTCVVVDV SQEDPEVQFN WYVDGVEVHN AKTKPREEQF NSTYRVVSVL  300
TVLHQDWLNG KEYKCKVSNK GLPSSIEKTI SKAKGQPREP QVYTLPPSQE EMTKNQVSLT  360
CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSRLTVDKSR WQEGNVFSCS  420
VMHEALHNHY TQKSLSLSLG                                              440

SEQ ID NO: 447          moltype = AA  length = 216
FEATURE                 Location/Qualifiers
source                  1..216
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 447
QSVLTQPPSA SGTPGQRVTI SCSGSTSNIG RESVYWYQQL PGTAPKLLIY LNSQRPSGVP  60
DRFSGSKSGT SASLAISGLQ SEDVADYYCG TWDDSLNGWV FGGGTKLTVL GQPKAAPSVT  120
LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS  180
YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS                             216

SEQ ID NO: 448          moltype = DNA  length = 6765
FEATURE                 Location/Qualifiers
source                  1..6765
                        mol_type = other DNA
                        organism = Synthetic construct
SEQUENCE: 448
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ggcgattaag ttgggtaacg ccagggtttt cccagtcacg acgttgtaaa acgacggcca  180
gtgccaagct gatctataca ttgaatcaat attggcaatt agccatatta gtcattggtt  240
atatagcata aatcaatatt ggctattggc cattgcatac gttgtatcta tatcataata  300
tgtacattta tattggctca tgtccaatat gaccgccatg ttgacattga ttattgacta  360
gttattaata gtaatcaatt acggggtcat tagttcatag cccatatatg gagttccgcg  420
ttacataact tacggtaaat ggcccgcctg gctgaccgcc caacgacccc cgcccattga  480
cgtcaataat gacgtatgtt cccatagtaa cgccaatagg gactttccat tgacgtcaat  540
gggtggagta tttacggtaa actgcccact tggcagtaca tcaagtgtat catatgccaa  600
gtccgccccc tattgacgtc aatgacggta aatggcccgc ctggcattat gcccagtaca  660
tgaccttacg ggactttcct acttggcagt acatctacgt attagtcatc gctattacca  720
tggtgatgcg gttttggcag tacaccaatg ggcgtggata gcggtttgac tcacggggat  780
ttccaagtct ccaccccatt gacgtcaatg ggagtttgtt ttggcaccaa aatcaacggg  840
actttccaaa atgtcgtaat aaccccgccc cgttgacgca aatgggcggt aggcgtgtac  900
ggtgggaggt ctatataagc agagctcgtt tagtgaaccg tcagaatttt gtaatacgac  960
tcactatagg gcggccggga attcgtcgac tggatccggt accgaggaga tctgccgccg  1020
cgatcgccgg cgcgccagat ctcaagctta tggacatgcg ggtgccagca caacttctcg  1080
gattactatt gttatggctg cgaggtgcgc gctgttatcc ttacgacgtg cctgactacg  1140
ccccaggatg gttcttagag tccccagaca ggccctggaa cgcccccacc ttctccccag  1200
ccctgctcct ggtgaccgaa ggggacaacg ccaccttcac ctgcagcttc tccaacgcat  1260
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ccgatcttag ccagacgagc gggttcggcc cattcggacc gcaaggaatc ggtcaataca  3240
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cctttgacgt tggagtccac gttctttaat agtggactct tgttccaaac tggaacaaca  6660
ctcaacccta tctcggtcta ttcttttgat ttataaggga ttttgccgat ttcggcctat  6720
tggttaaaaa atgagctgat ttaacaaaaa tttaacgcga atttt                  6765

SEQ ID NO: 449         moltype = AA  length = 447
FEATURE                Location/Qualifiers
source                 1..447
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 449
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AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS  120
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFLGGPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT  360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE  420
GNVFSCSVMH EALHNHYTQK SLSLSLG                                      447

SEQ ID NO: 450         moltype = AA  length = 215
FEATURE                Location/Qualifiers
source                 1..215
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                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 450
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SRFSGSGSGT DFTLTINSLE AEDAATYYCH QFHSSPLTFG GGTKLEIKRT VAAPSVFIFP  120
PSDEQLKSGT ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL  180
TLSKADYEKH KVYACEVTHQ GLSSPVTKSF NRGEC                            215

SEQ ID NO: 451       moltype = AA  length = 579
FEATURE              Location/Qualifiers
source               1..579
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 451
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ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCATND DYWGQGTLVT VSSASTKGPS  120
VFPLAPCSRS TSESTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS  180
VVTVPSSSLG TKTYTCNVDH KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP  240
KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN STYRVVSVLT  300
VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ VYTLPPSQEE MTKNQVSLTC  360
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV  420
MHEALHNHYT QKSLSLSLGK SGGGGSAPTS SSTKKTQLQL EHLLLALQMI LNGINNYKNP  480
KLTEMLTFKF YMPKKATELK HLQCLEEELK PLEEVLNLAQ SKNFHLRPRD LISNINVIVL  540
ELKGSETTFM CEYADETATI VEFLNRWITF CQSIISTLT                         579

SEQ ID NO: 452       moltype = AA  length = 214
FEATURE              Location/Qualifiers
source               1..214
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 452
EIVLTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA  60
RFSGSGSGTD FTLTISSLEP EDFAVYYCQQ SSNWPRTFGQ GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 453       moltype = AA  length = 588
FEATURE              Location/Qualifiers
source               1..588
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 453
EVQLLESGGG LVQPGGSLRL SCAASGFTFS SNYMSWVRQA PGKGLEWVSA ISSSGGTIFY  60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKHK WNAVYYDGMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKS GGGGSAPTSS STKKTQLQLE HLLLALQMIL  480
NGINNYKNPK LTEMLTFKFY MPKKATELKH LQCLEEELKP LEEVLNLAQS KNFHLRPRDL  540
ISNINVIVLE LKGSETTFMC EYADETATIV EFLNRWITFC QSIISTLT                588

SEQ ID NO: 454       moltype = AA  length = 585
FEATURE              Location/Qualifiers
source               1..585
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 454
EVQLLESGGG LVQPGGSLRL SCTASGFTFS SYEMQWVRQA PGKGLEWVLG ITSSSSHIFY  60
ADSVKGRFTV SRDNSKNTLY LQMNSLRAED TAVYYCTKDL NSYYGLDVWG QGTTVTVSSA  120
STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTKTY TCNVDHKPSN TKVDKRVESK YGPPCPPCPA PEFLGGPSVF  240
LFPPKPKDTL MISRTPEVTC VVVDVSQEDP EVQFNWYVDG VEVHNAKTKP REEQFNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKGLPSS IEKTISKAKG QPREPQVYTL PPSQEEMTKN  360
QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT VDKSRWQEGN  420
VFSCSVMHEA LHNHYTQKSL SLSLGKSGGG GSAPTSSSTK KTQLQLEHLL LALQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN  540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                  585

SEQ ID NO: 455       moltype = AA  length = 588
FEATURE              Location/Qualifiers
source               1..588
                     mol_type = protein
                     organism = Synthetic construct
SEQUENCE: 455
EVQLLESGGG LVQPGGSLRL SCAASGFTFS DYYMSWVRQA PGKGLEWVSA ISSSGGTIFY  60
ADSVKGRFII SRDNSKNTLY LQMNSLRAED TAVYYCAKHK WNDVYYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
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SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKS GGGGSAPTSS STKKTQLQLE HLLLALQMIL  480
NGINNYKNPK LTEMLTFKFY MPKKATELKH LQCLEEELKP LEEVLNLAQS KNFHLRPRDL  540
ISNINVIVLE LKGSETTFMC EYADETATIV EFLNRWITFC QSIISTLT                588

SEQ ID NO: 456         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 456
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTE  480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                             575

SEQ ID NO: 457         moltype = AA  length = 574
FEATURE                Location/Qualifiers
source                 1..574
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 457
DSLVESGGGL VQPGGSLRLS CAASGFTFDI SAMSWVRQAP GKGLEWVSTI SGSAYSTYYA  60
DSVKGRFTIS RDNSKSTLYL QMNSLRAEDT AVYYCAREIF SDYWGLGTLV TVSSASTKGP  120
SVFPLAPCSR STSESTAALG CLVKDYFPEP VTVSWNSGAL TSGVHTFPAV LQSSGLYSLS  180
SVVTVPSSSL GTKTYTCNVD HKPSNTKVDK RVESKYGPPC PPCPAPEFLG GPSVFLFPPK  240
PKDTLMISRT PEVTCVVVDV SQEDPEVQFN WYVDGVEVHN AKTKPREEQF NSTYRVVSVL  300
TVLHQDWLNG KEYKCKVSNK GLPSSIEKTI SKAKGQPREP QVYTLPPSQE EMTKNQVSLT  360
CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSRLTVDKSR WQEGNVFSCS  420
VMHEALHNHY TQKSLSLSLG KAPTSSSTKK TQLQLEHLLL ALQMILNGIN NYKNPKLTEM  480
LTFKFYMPKK ATELKHLQCL EEELKPLEEV LNLAQSKNFH LRPRDLISNI NVIVLELKGS  540
ETTFMCEYAD ETATIVEFLN RWITFCQSII STLT                              574

SEQ ID NO: 458         moltype = AA  length = 448
FEATURE                Location/Qualifiers
source                 1..448
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 458
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFEGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLG                                     448

SEQ ID NO: 459         moltype = AA  length = 448
FEATURE                Location/Qualifiers
source                 1..448
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 459
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFAGAP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLG                                     448

SEQ ID NO: 460         moltype = AA  length = 448
FEATURE                Location/Qualifiers
source                 1..448
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 460
EVQLLESGGC LVQPGGSLRL SCAASGFTFS DYYMSWVRQA PGKGLEWVSA ISSSGGTIFY  60
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ADSVKGRFII SRDNSKNTLY LQMNSLRAED TAVYYCAKHK WNDVYYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLG                                     448

SEQ ID NO: 461         moltype = AA  length = 441
FEATURE                Location/Qualifiers
source                 1..441
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 461
DMQLVESGGG VVRPGESLRL SCTASGFTFS ISAMSWVRQA PGKGLEWVSA ISGTAYSTYY  60
ADSVRGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDN FFDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL G                                            441

SEQ ID NO: 462         moltype = AA  length = 216
FEATURE                Location/Qualifiers
source                 1..216
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 462
QSVMTQPPSA SGTPGQRVTI SCSGVTSNIG SNSVYWYQQL PGTAPKLLIY LNSQRPSGVP  60
DRFSGSKSGT SASLAISGLQ SEDEADYYCG TWDDSLNGWV FGGGTKLTVL GQPKAAPSVT  120
LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS  180
YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS                            216

SEQ ID NO: 463         moltype = AA  length = 441
FEATURE                Location/Qualifiers
source                 1..441
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 463
DVQLVESGGG VVRPGESLRL SCTASGFTFS ISAMSWVRQA PGKGLEWVSA ISGTAYSTYY  60
ADSVRGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDN FFDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL G                                            441

SEQ ID NO: 464         moltype = AA  length = 441
FEATURE                Location/Qualifiers
source                 1..441
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 464
DVQLVESGGG VVRPGGSLRL SCAASGFTFS IYAMSWVRQA PGEGLEWVSH ISASGGSTYY  60
ADSVKGRFAI SRDNSKNTLY LQMNSLRAED TAVYYCTTNL GSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL G                                            441

SEQ ID NO: 465         moltype = AA  length = 441
FEATURE                Location/Qualifiers
source                 1..441
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 465
DVQLVESGGG VVRPGGSLRL SCAASGFTFS IYAVSWVRQA PGEGLEWVSH ISASGGSTYY  60
ADSVKGRFAI SRDNSKNTLY LQMNSLRAED TAVYYCTTNL GSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL G                                            441
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SEQ ID NO: 466 moltype = AA length = 216
FEATURE Location/Qualifiers
source 1..216
mol_type = protein
organism = Synthetic construct
SEQUENCE: 466
QSVLTQPPSA SGTPGQRVTI SCSGSYSDIG TNYVYWYQQL PGTAPKLLIF ATDRRPSGVP 60
DRFSGSKSGT SASLAISGLQ SEDEADYYCG TWDDSLNVWV FGGGTKLTVL GQPKAAPSVT 120
LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS 180
YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS 216

SEQ ID NO: 467 moltype = AA length = 443
FEATURE Location/Qualifiers
source 1..443
mol_type = protein
organism = Synthetic construct
SEQUENCE: 467
DVQLVESGGG VVRPGESLRL SCAASGFTFS TDAMGWVRQA PGEGLEWVSL ISGSGYSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLTAED TAVYYCAKNS LAFFDYWGLG TLVTVSSAST 120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF 240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV 360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF 420
SCSVMHEALH NHYTQKSLSL SLG 443

SEQ ID NO: 468 moltype = AA length = 216
FEATURE Location/Qualifiers
source 1..216
mol_type = protein
organism = Synthetic construct
SEQUENCE: 468
QSVLTQPPSA SGTPGQRVTI SCSGGSSNIG RESVNWYQQL PGTAPKLLIY STDRRPSGVP 60
DRFSGSKSGT SASLAISGLQ SEDEADYYCG TWDNDLNGWV FGGGTKLTVL GQPKAAPSVT 120
LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS 180
YLSLTPEQWK SHRSYSCQVT HEGSTVEKTV APTECS 216

SEQ ID NO: 469 moltype = AA length = 449
FEATURE Location/Qualifiers
source 1..449
mol_type = protein
organism = Synthetic construct
SEQUENCE: 469
DVQLQESGPG LVKPSQSLSL TCTVTGHSIT SDYAWNWIRQ FPGDKLEWMG YISYSGYTTY 60
NPSLKSRVSI TRDTSKNQFF LQLNSVTTED TATYFCARDL DYGPWFAYWG QGTLVTVSAA 120
STKGPSVFPL APSSKSTSGG TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG 180
LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP 240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSRDEL 360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ 420
QGNVFSCSVM HEALHNHYTQ KSLSLSPGK 449

SEQ ID NO: 470 moltype = AA length = 214
FEATURE Location/Qualifiers
source 1..214
mol_type = protein
organism = Synthetic construct
SEQUENCE: 470
DIQMTQSPAS LSASVGETVT LTCRASENIH NYLAWYQQKQ GKSPQLLVYN VKTLADGVPS 60
RFSGSGSGTQ YSLKINSLQP EDFGSYYCQH FWSSPWTFGG GTKVEIKRTV AAPSVFIFPP 120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT 180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC 214

SEQ ID NO: 471 moltype = AA length = 585
FEATURE Location/Qualifiers
source 1..585
mol_type = protein
organism = Synthetic construct
SEQUENCE: 471
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA 240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LALQMILNGI 480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN 540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT 585

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SEQ ID NO: 472 moltype = AA length = 582
FEATURE Location/Qualifiers
source 1..582
mol_type = protein
organism = Synthetic construct
SEQUENCE: 472
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFEGGP 240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM 360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ 420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLAL QMILNGINNY 480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV 540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT 582

SEQ ID NO: 473 moltype = AA length = 582
FEATURE Location/Qualifiers
source 1..582
mol_type = protein
organism = Synthetic construct
SEQUENCE: 473
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFAGAP 240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM 360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ 420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLAL QMILNGINNY 480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV 540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT 582

SEQ ID NO: 474 moltype = AA length = 585
FEATURE Location/Qualifiers
source 1..585
mol_type = protein
organism = Synthetic construct
SEQUENCE: 474
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA 240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI 480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN 540
INVKVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT 585

SEQ ID NO: 475 moltype = AA length = 582
FEATURE Location/Qualifiers
source 1..582
mol_type = protein
organism = Synthetic construct
SEQUENCE: 475
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFEGGP 240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM 360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ 420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLDL QMILNGINNY 480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV 540
KVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT 582

SEQ ID NO: 476 moltype = AA length = 582
FEATURE Location/Qualifiers
source 1..582
mol_type = protein
organism = Synthetic construct
SEQUENCE: 476
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFAGAP 240

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SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLDL QMILNGINNY  480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV  540
KVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT                      582

SEQ ID NO: 477         moltype = AA  length = 585
FEATURE                Location/Qualifiers
source                 1..585
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 477
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA  240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRKLISN  540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                   585

SEQ ID NO: 478         moltype = AA  length = 582
FEATURE                Location/Qualifiers
source                 1..582
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 478
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFEGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLDL QMILNGINNY  480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRKLISNINV  540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT                      582

SEQ ID NO: 479         moltype = AA  length = 582
FEATURE                Location/Qualifiers
source                 1..582
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 479
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFAGAP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLDL QMILNGINNY  480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRKLISNINV  540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT                      582

SEQ ID NO: 480         moltype = AA  length = 577
FEATURE                Location/Qualifiers
source                 1..577
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 480
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKAPTSSS TKKTQLQLEH LLLDLQMILN GINNYKNPKL  480
TRMLTFKFYM PKKATELKHL QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL  540
KGSETTFMCE YADETATIVE FLNRWITFCQ SIISTLT                            577

SEQ ID NO: 481         moltype = AA  length = 583
FEATURE                Location/Qualifiers
source                 1..583
                       mol_type = protein
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organism = Synthetic construct

SEQUENCE: 481

EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF 240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV 360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF 420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLD LQMILNGINN 480
YKNPKLTRML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN 540
VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT 583

SEQ ID NO: 482 moltype = AA length = 443

FEATURE Location/Qualifiers

source 1..443

mol_type = protein

organism = Synthetic construct

SEQUENCE: 482

EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF 240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV 360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF 420
SCSVMHEALH NHYTQKSLSL SLG 443

SEQ ID NO: 483 moltype = AA length = 346

FEATURE Location/Qualifiers

source 1..346

mol_type = protein

organism = Synthetic construct

SEQUENCE: 483

DTVLTQSPAL AVSPGERVTI SCRASESVRT GVHWYQQKPG QQPKLLIYGA SNLESGVPAR 60
FSGSGSGTDF TLTIDPVEAD DTATYFCQQS WNDPFTFGSG TKLEIKRTVA APSVFIFPPS 120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL 180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GECAPTSSST KKTQLQLEHL LLDLQMILNG 240
INNYKNPKLT RMLTFKFYMP KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS 300
NINVIVLELK GSETTFMCEY ADETATIVEF LNRWITFCQS IISTLT 346

SEQ ID NO: 484 moltype = AA length = 352

FEATURE Location/Qualifiers

source 1..352

mol_type = protein

organism = Synthetic construct

SEQUENCE: 484

DTVLTQSPAL AVSPGERVTI SCRASESVRT GVHWYQQKPG QQPKLLIYGA SNLESGVPAR 60
FSGSGSGTDF TLTIDPVEAD DTATYFCQQS WNDPFTFGSG TKLEIKRTVA APSVFIFPPS 120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL 180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GECSGGGGSA PTSSSTKKTQ LQLEHLLLDL 240
QMILNGINNY KNPKLTRMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR 300
PRDLISNINV IVLELKGSET TFMCEYADET ATIVEFLNRW ITFCQSIIST LT 352

SEQ ID NO: 485 moltype = AA length = 583

FEATURE Location/Qualifiers

source 1..583

mol_type = protein

organism = Synthetic construct

SEQUENCE: 485

EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF 240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV 300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV 360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF 420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLY LQMILNGINN 480
YKNPKLTRML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN 540
VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT 583

SEQ ID NO: 486 moltype = AA length = 577

FEATURE Location/Qualifiers

source 1..577

mol_type = protein

organism = Synthetic construct

SEQUENCE: 486

EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120

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KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKAPTSSS TKKTQLQLEH LLLYLQMILN GINNYKNPKL  480
TRMLTFKFYM PKKATELKHL QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL  540
KGSETTFMCE YADETATIVE FLNRWITFCQ SIISTLT                           577

SEQ ID NO: 487         moltype = AA  length = 580
FEATURE                Location/Qualifiers
source                 1..580
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 487
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKAPT SSSTKKTQLQ LEHLLLYLQM ILNGINNYKN  480
PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR DLISNINVIV  540
LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT                        580

SEQ ID NO: 488         moltype = AA  length = 583
FEATURE                Location/Qualifiers
source                 1..583
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 488
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLA LQMILNGINN  480
YKNPKLTPML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT                    583

SEQ ID NO: 489         moltype = AA  length = 583
FEATURE                Location/Qualifiers
source                 1..583
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 489
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLA LQMILNGINN  480
YKNPKLTSML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT                    583

SEQ ID NO: 490         moltype = AA  length = 583
FEATURE                Location/Qualifiers
source                 1..583
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 490
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLA LQMILNGINN  480
YKNPKLTDML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT                    583

SEQ ID NO: 491         moltype = AA  length = 583
FEATURE                Location/Qualifiers
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source                  1..583
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 491
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLA LQMILNGINN  480
YKNPKLTQML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VIVLALKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT                     583

SEQ ID NO: 492          moltype = AA  length = 583
FEATURE                 Location/Qualifiers
source                  1..583
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 492
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLA LQMILNGINN  480
YKNPKLTRML THKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VIVLALKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT                     583

SEQ ID NO: 493          moltype = AA  length = 583
FEATURE                 Location/Qualifiers
source                  1..583
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 493
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLD LQMILNGINN  480
YKNPKLTDML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VDVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT                     583

SEQ ID NO: 494          moltype = AA  length = 583
FEATURE                 Location/Qualifiers
source                  1..583
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 494
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLD LQMILNGINN  480
YKNPKLTEML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VDVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT                     583

SEQ ID NO: 495          moltype = AA  length = 583
FEATURE                 Location/Qualifiers
source                  1..583
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 495
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
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SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLD LQMILNGINN  480
YKNPKLTRML THKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VDVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT                    583

SEQ ID NO: 496         moltype = AA  length = 583
FEATURE                Location/Qualifiers
source                 1..583
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 496
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APTSSSTKKT QLQLEHLLLA LQMILNGINN  480
YKNPKLTEML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT                    583

SEQ ID NO: 497         moltype = AA  length = 583
FEATURE                Location/Qualifiers
source                 1..583
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 497
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APASSSTKKT QLQLEHLLLA LQMILNGINN  480
YKNPKLTEML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFCQSIIS TLT                    583

SEQ ID NO: 498         moltype = AA  length = 583
FEATURE                Location/Qualifiers
source                 1..583
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 498
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APASSSTKKT QLQLEHLLLA LQMILNGINN  480
YKNPKLTEML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFAQSIIS TLT                    583

SEQ ID NO: 499         moltype = AA  length = 583
FEATURE                Location/Qualifiers
source                 1..583
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 499
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKSGGGGS APASSSTKKT QLQLEHLLLA LQMILNGINN  480
YKNPKLTEML TFKFYMPKKA TELKHLQCLE EELKPLEEVL NLAQSKNFHL RPRDLISNIN  540
VIVLELKGSE TTFMCEYADE TATIVEFLNR WITFAQSIIS TLT                    583

SEQ ID NO: 500         moltype = AA  length = 586
FEATURE                Location/Qualifiers
source                 1..586
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 500
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
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RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSAPTSSST KKTQLQLEHL LLALQMILNG  480
INNYKNPKLT EMLTFKFYMP KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS  540
NINVIVLELK GSETTFMCEY ADETATIVEF LNRWITFCQS IISTLT                  586

SEQ ID NO: 501         moltype = AA  length = 586
FEATURE                Location/Qualifiers
source                 1..586
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 501
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSAPASSST KKTQLQLEHL LLALQMILNG  480
INNYKNPKLT EMLTFKFYMP KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS  540
NINVIVLELK GSETTFMCEY ADETATIVEF LNRWITFCQS IISTLT                  586

SEQ ID NO: 502         moltype = AA  length = 586
FEATURE                Location/Qualifiers
source                 1..586
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 502
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSAPTSSST KKTQLQLEHL LLALQMILNG  480
INNYKNPKLT EMLTFKFYMP KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS  540
NINVIVLELK GSETTFMCEY ADETATIVEF LNRWITFAQS IISTLT                  586

SEQ ID NO: 503         moltype = AA  length = 346
FEATURE                Location/Qualifiers
source                 1..346
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 503
DTVLTQSPAL AVSPGERVTI SCRASESVRT GVHWYQQKPG QQPKLLIYGA SNLESGVPAR  60
FSGSGSGTDF TLTIDPVEAD DTATYFCQQS WNDPFTFGSG TKLEIKRTVA APSVFIFPPS  120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL  180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GECAPTSSST KKTQLQLEHL LLALQMILNG  240
INNYKNPKLT EMLTFKFYMP KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS  300
NINVIVLELK GSETTFMCEY ADETATIVEF LNRWITFCQS IISTLT                  346

SEQ ID NO: 504         moltype = AA  length = 352
FEATURE                Location/Qualifiers
source                 1..352
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 504
DTVLTQSPAL AVSPGERVTI SCRASESVRT GVHWYQQKPG QQPKLLIYGA SNLESGVPAR  60
FSGSGSGTDF TLTIDPVEAD DTATYFCQQS WNDPFTFGSG TKLEIKRTVA APSVFIFPPS  120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL  180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GECSGGGGSA PTSSSTKKTQ LQLEHLLLAL  240
QMILNGINNY KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR  300
PRDLISNINV IVLELKGSET TFMCEYADET ATIVEFLNRW ITFCQSIIST LT           352

SEQ ID NO: 505         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 505
DVQLVESGGG VVRPGESLRL SCTASGFTFS ISAMSWVRQA PGKGLEWVSA ISGTAYSTYY  60
ADSVRGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKDN FFDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
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SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTE  480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                             575

SEQ ID NO: 506         moltype = AA  length = 577
FEATURE                Location/Qualifiers
source                 1..577
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 506
DVQLVESGGG VVRPGESLRL SCAASGFTFS TDAMGWVRQA PGEGLEWVSL ISGSGYSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNSLTAED TAVYYCAKNS LAFFDYWGLG TLVTVSSAST  120
KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTKTYTC NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF  240
PPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV  300
SVLTVLHQDW LNGKEYKCKV SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV  360
SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPPVLDSDGS FFLYSRLTVD KSRWQEGNVF  420
SCSVMHEALH NHYTQKSLSL SLGKAPTSSS TKKTQLQLEH LLLALQMILN GINNYKNPKL  480
TEMLTFKFYM PKKATELKHL QCLEEELKPL EEVLNLAQSK NFHLRPRDLI SNINVIVLEL  540
KGSETTFMCE YADETATIVE FLNRWITFCQ SIISTLT                           577

SEQ ID NO: 507         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 507
DVQLVESGGG VVRPGGSLRL SCAASGFTFS IYAMSWVRQA PGEGLEWVSH ISASGGSTYY  60
ADSVKGRFAI SRDNSKNTLY LQMNSLRAED TAVYYCTTNL GSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTE  480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                             575

SEQ ID NO: 508         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 508
DVQLVESGGG VVRPGGSLRL SCAASGFTFS IYAVSWVRQA PGEGLEWVSH ISASGGSTYY  60
ADSVKGRFAI SRDNSKNTLY LQMNSLRAED TAVYYCTTNL GSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTE  480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                             575

SEQ ID NO: 509         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 509
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTR  480
MLTAKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                             575

SEQ ID NO: 510         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
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mol_type = protein
organism = Synthetic construct

SEQUENCE: 510

DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY 60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG 120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL 180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP 240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL 360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC 420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTR 480
MLTSKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG 540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT 575

SEQ ID NO: 511 moltype = AA length = 575
FEATURE Location/Qualifiers
source 1..575
mol_type = protein
organism = Synthetic construct

SEQUENCE: 511

DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY 60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG 120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL 180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP 240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL 360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC 420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LSLQMILNGI NNYKNPKLTE 480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG 540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT 575

SEQ ID NO: 512 moltype = AA length = 575
FEATURE Location/Qualifiers
source 1..575
mol_type = protein
organism = Synthetic construct

SEQUENCE: 512

DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY 60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG 120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL 180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP 240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL 360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC 420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LDLQMILNGI NNYKNPKLTR 480
MLTAKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISR INVIVLELKG 540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT 575

SEQ ID NO: 513 moltype = AA length = 575
FEATURE Location/Qualifiers
source 1..575
mol_type = protein
organism = Synthetic construct

SEQUENCE: 513

DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY 60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG 120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL 180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP 240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL 360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC 420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LDLQMILNGI NNYKNPKLTR 480
MLTIKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVDVLELKG 540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT 575

SEQ ID NO: 514 moltype = AA length = 575
FEATURE Location/Qualifiers
source 1..575
mol_type = protein
organism = Synthetic construct

SEQUENCE: 514

DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY 60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG 120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL 180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP 240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV 300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL 360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC 420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LDLQMILNGI NNYKNPKLTR 480

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MLTQKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVDVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                            575

SEQ ID NO: 515         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 515
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LDLQMILNGI NNYKNPKLTR  480
MLTTKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVDVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                            575

SEQ ID NO: 516         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 516
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LDLQMILNGI NNYKNPKLTR  480
MLTWKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVDVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                            575

SEQ ID NO: 517         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 517
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LDLQMILNGI NNYKNPKLTE  480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRKLISN INVIVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                            575

SEQ ID NO: 518         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 518
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPTSSSTK KTQLQLEHLL LDLQMILNGI NNYKNPKLTE  480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVKVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT                            575

SEQ ID NO: 519         moltype = AA  length = 581
FEATURE                Location/Qualifiers
source                 1..581
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 519
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY  60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS  120
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SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFLGGPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT  360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE  420
GNVFSCSVMH EALHNHYTQK SLSLSLGKAP TSSSTKKTQL QLEHLLLALQ MILNGINNYK  480
NPKLTEMLTF KFYMPKKATE LKHLQCLEEE LKPLEEVLNL AQSKNFHLRP RDLISNINVI  540
VLELKGSETT FMCEYADETA TIVEFLNRWI TFCQSIISTL T                       581

SEQ ID NO: 520         moltype = AA  length = 581
FEATURE                Location/Qualifiers
source                 1..581
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 520
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY  60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS  120
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFEGGPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT  360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE  420
GNVFSCSVMH EALHNHYTQK SLSLSLGKAP ASSSTKKTQL QLEHLLLALQ MILNGINNYK  480
NPKLTEMLTF KFYMPKKATE LKHLQCLEEE LKPLEEVLNL AQSKNFHLRP RDLISNINVI  540
VLELKGSETT FMCEYADETA TIVEFLNRWI TFAQSIISTL T                       581

SEQ ID NO: 521         moltype = AA  length = 581
FEATURE                Location/Qualifiers
source                 1..581
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 521
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY  60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS  120
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFAGAPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT  360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE  420
GNVFSCSVMH EALHNHYTQK SLSLSLGKAP ASSSTKKTQL QLEHLLLALQ MILNGINNYK  480
NPKLTEMLTF KFYMPKKATE LKHLQCLEEE LKPLEEVLNL AQSKNFHLRP RDLISNINVI  540
VLELKGSETT FMCEYADETA TIVEFLNRWI TFAQSIISTL T                       581

SEQ ID NO: 522         moltype = AA  length = 586
FEATURE                Location/Qualifiers
source                 1..586
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 522
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELAGAPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSAPASSST KKTQLQLEHL LLALQMILNG  480
INNYKNPKLT EMLTFKFYMP KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS  540
NINVIVLELK GSETTFMCEY ADETATIVEF LNRWITFAQS IISTLT                  586

SEQ ID NO: 523         moltype = AA  length = 216
FEATURE                Location/Qualifiers
source                 1..216
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 523
EIVLTQSPGT LSLSPGERAT LSCRASQSIG RSFLAWYQQK PGQAPRLLIY DASTRAADIP  60
ARFSGSGSGT DFTLTISSLE PEDFAVYYCQ QYYDWPPLSF GGGTKVEIKR TVAAPSVFIF  120
PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST  180
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC                             216

SEQ ID NO: 524         moltype = AA  length = 582
FEATURE                Location/Qualifiers
source                 1..582
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 524
EVQLLESGGG LVQPGGSLRL SCVGSGFNLK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYT RGSYFYDAMD VWGQGTTVTV  120
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SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PTSSSTKKTQ LQLEHLLLAL QMILNGINNY  480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV  540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFCQSIIST LT                      582

SEQ ID NO: 525         moltype = AA  length = 216
FEATURE                Location/Qualifiers
source                 1..216
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 525
EIVLTQSPGT LSLSPGERAT LSCRASQSIG RSFLAWYQQK PGQAPRLLIY DASTRAADIP  60
DRFSGSGSGT DFTLTINRLE PEDFAVYYCQ QYYDWPPLTF GGGTKVEIKR TVAAPSVFIF  120
PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST  180
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC                             216

SEQ ID NO: 526         moltype = AA  length = 582
FEATURE                Location/Qualifiers
source                 1..582
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 526
EVQLLESGGG LVQPGGSLRL SCVGSGFNFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYT RGSYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PTSSSTKKTQ LQLEHLLLAL QMILNGINNY  480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV  540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFCQSIIST LT                      582

SEQ ID NO: 527         moltype = AA  length = 216
FEATURE                Location/Qualifiers
source                 1..216
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 527
EIVLTQSPGT LSLSPGERAT LSCRASQSIG RSFLAWYQQK PGQAPRLLIY DASTRATDIP  60
DRFSGSGSGT EFTLTISSLQ SEDFAVYYCQ QYYDWPPLTF GGGTKVEIKR TVAAPSVFIF  120
PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST  180
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC                             216

SEQ ID NO: 528         moltype = AA  length = 582
FEATURE                Location/Qualifiers
source                 1..582
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 528
EVQLLESGGG LVQPGGSLRL SCVGSGFNFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYT RGSYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFEGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLAL QMILNGINNY  480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV  540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT                      582

SEQ ID NO: 529         moltype = AA  length = 582
FEATURE                Location/Qualifiers
source                 1..582
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 529
EVQLLESGGG LVQPGGSLRL SCVGSGFNFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYT RGSYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFAGAP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLAL QMILNGINNY  480
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KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV 540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT 582

SEQ ID NO: 530 moltype = AA length = 585
FEATURE Location/Qualifiers
source 1..585
mol_type = protein
organism = Synthetic construct
SEQUENCE: 530
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELL 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LALQMILNGI 480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN 540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT 585

SEQ ID NO: 531 moltype = AA length = 585
FEATURE Location/Qualifiers
source 1..585
mol_type = protein
organism = Synthetic construct
SEQUENCE: 531
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELE 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LALQMILNGI 480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN 540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT 585

SEQ ID NO: 532 moltype = AA length = 585
FEATURE Location/Qualifiers
source 1..585
mol_type = protein
organism = Synthetic construct
SEQUENCE: 532
EVQLLESGGG LVQPGGSLRL SCAASGFTFK SYAMHWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKYD RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA 240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LALQMILNGI 480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN 540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT 585

SEQ ID NO: 533 moltype = AA length = 585
FEATURE Location/Qualifiers
source 1..585
mol_type = protein
organism = Synthetic construct
SEQUENCE: 533
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ 180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELE 240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ 300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR 360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS 420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI 480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRKLISN 540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT 585

SEQ ID NO: 534 moltype = AA length = 582
FEATURE Location/Qualifiers
source 1..582
mol_type = protein
organism = Synthetic construct
SEQUENCE: 534
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV 120

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SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLDL QMILNGINNY  480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRKLISNINV  540
IVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT                      582

SEQ ID NO: 535         moltype = AA  length = 585
FEATURE                Location/Qualifiers
source                 1..585
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 535
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELL  240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN  540
INVKVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                   585

SEQ ID NO: 536         moltype = AA  length = 585
FEATURE                Location/Qualifiers
source                 1..585
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 536
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELE  240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN  540
INVKVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                   585

SEQ ID NO: 537         moltype = AA  length = 582
FEATURE                Location/Qualifiers
source                 1..582
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 537
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPCSRST SESTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM  360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ  420
EGNVFSCSVM HEALHNHYTQ KSLSLSLGKA PASSSTKKTQ LQLEHLLLDL QMILNGINNY  480
KNPKLTEMLT FKFYMPKKAT ELKHLQCLEE ELKPLEEVLN LAQSKNFHLR PRDLISNINV  540
KVLELKGSET TFMCEYADET ATIVEFLNRW ITFAQSIIST LT                      582

SEQ ID NO: 538         moltype = AA  length = 585
FEATURE                Location/Qualifiers
source                 1..585
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 538
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA  240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LSLQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN  540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                   585

SEQ ID NO: 539         moltype = AA  length = 585
FEATURE                Location/Qualifiers
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source                  1..585
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 539
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA  240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRFLISN  540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                   585

SEQ ID NO: 540          moltype = AA  length = 585
FEATURE                 Location/Qualifiers
source                  1..585
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 540
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA  240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN  540
INVRVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                   585

SEQ ID NO: 541          moltype = AA  length = 585
FEATURE                 Location/Qualifiers
source                  1..585
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 541
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA  240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN  540
INVEVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                   585

SEQ ID NO: 542          moltype = AA  length = 585
FEATURE                 Location/Qualifiers
source                  1..585
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 542
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA  240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN  540
INVSVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                   585

SEQ ID NO: 543          moltype = AA  length = 585
FEATURE                 Location/Qualifiers
source                  1..585
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 543
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA  240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
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RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEHLL LDLQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN  540
INVDVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                  585

SEQ ID NO: 544         moltype = AA  length = 585
FEATURE                Location/Qualifiers
source                 1..585
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 544
EVQLLESGGG LVQPGGSLRL SCAASGFTFK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY  60
ADSVKGRFTI SRDNSKNTLY LQMNNLRAED TAVYYCAKYT RASYFYDAMD VWGQGTTVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELA  240
GAPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKAPASSSTK KTQLQLEELL LDLQMILNGI  480
NNYKNPKLTE MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN  540
INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                  585

SEQ ID NO: 545         moltype = AA  length = 586
FEATURE                Location/Qualifiers
source                 1..586
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 545
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSAPASSST KKTQLQLEHL LLALQMILNG  480
INNYKNPKLT EMLTFKFYMP KKATELKHLQ CLEEELKPLE EVLNLAQSKN FHLRPRDLIS  540
NINVIVLELK GSETTFMCEY ADETATIVEF LNRWITFAQS IISTLT                  586

SEQ ID NO: 546         moltype = AA  length = 580
FEATURE                Location/Qualifiers
source                 1..580
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 546
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELAGAPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKAPA SSSTKKTQLQ LEHLLLALQM ILNGINNYKN  480
PKLTEMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR DLISNINVIV  540
LELKGSETTF MCEYADETAT IVEFLNRWIT FAQSIISTLT                        580

SEQ ID NO: 547         moltype = AA  length = 447
FEATURE                Location/Qualifiers
source                 1..447
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 547
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY  60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS  120
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFEGGPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT  360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE  420
GNVFSCSVMH EALHNHYTQK SLSLSLG                                      447

SEQ ID NO: 548         moltype = AA  length = 447
FEATURE                Location/Qualifiers
source                 1..447
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 548
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY  60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS  120
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
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SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFAGAPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT  360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE  420
GNVFSCSVMH EALHNHYTQK SLSLSLG                                      447

SEQ ID NO: 549         moltype = AA  length = 447
FEATURE                Location/Qualifiers
source                 1..447
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 549
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY  60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS  120
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFEGGPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLG SSIEKTISKA KGQPREPQVY TLPPSQEEMT  360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE  420
GNVFSCSVMH EALHNHYTQK SLSLSLG                                      447

SEQ ID NO: 550         moltype = AA  length = 581
FEATURE                Location/Qualifiers
source                 1..581
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 550
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY  60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS  120
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFLGGPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY TLPPSQEEMT  360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE  420
GNVFSCSVMH EALHNHYTQK SLSLSLGKAP ASSSTKKTQL QLEHLLLALQ MILNGINNYK  480
NPKLTEMLTF KFYMPKKATE LKHLQCLEEE LKPLEEVLNL AQSKNFHLRP RDLISNINVI  540
VLELKGSETT FMCEYADETA TIVEFLNRWI TFAQSIISTL T                      581

SEQ ID NO: 551         moltype = AA  length = 581
FEATURE                Location/Qualifiers
source                 1..581
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 551
QVQLVQSGSE LKKPGASVKV SCKASGYSLY GTSMHWVRQA PGQGLEWMGY ISPFTGRATY  60
AQGFTGRFVF SLDTSVSTAY LQISSLKAED TAVYYCARDY DYRYYYAMDY WGQGTTVTVS  120
SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTK TYTCNVDHKP SNTKVDKRVE SKYGPPCPPC PAPEFEGGPS  240
VFLFPPKPKD TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST  300
YRVVSVLTVL HQDWLNGKEY KCKVSNKGLG SSIEKTISKA KGQPREPQVY TLPPSQEEMT  360
KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD SDGSFFLYSR LTVDKSRWQE  420
GNVFSCSVMH EALHNHYTQK SLSLSLGKAP ASSSTKKTQL QLEHLLLALQ MILNGINNYK  480
NPKLTEMLTF KFYMPKKATE LKHLQCLEEE LKPLEEVLNL AQSKNFHLRP RDLISNINVI  540
VLELKGSETT FMCEYADETA TIVEFLNRWI TFAQSIISTL T                      581

SEQ ID NO: 552         moltype = AA  length = 441
FEATURE                Location/Qualifiers
source                 1..441
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 552
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFE GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL G                                            441

SEQ ID NO: 553         moltype = AA  length = 441
FEATURE                Location/Qualifiers
source                 1..441
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 553
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
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SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFA GAPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL G                                            441

SEQ ID NO: 554         moltype = AA  length = 441
FEATURE                Location/Qualifiers
source                 1..441
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 554
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFE GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLGSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL G                                            441

SEQ ID NO: 555         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 555
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFL GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPASSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTE  480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                              575

SEQ ID NO: 556         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 556
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFE GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPASSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTE  480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                              575

SEQ ID NO: 557         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 557
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFA GAPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPASSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTE  480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                              575

SEQ ID NO: 558         moltype = AA  length = 575
FEATURE                Location/Qualifiers
source                 1..575
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 558
DVQLVESGGG LVQPGGSLRL SCAASGFTFD ISAMSWVRQA PGKGLEWVST ISGSAYSTYY  60
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ADSVKGRFTI SRDNSKSTLY LQMNSLRAED TAVYYCAREI FSDYWGLGTL VTVSSASTKG  120
PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL  180
SSVVTVPSSS LGTKTYTCNV DHKPSNTKVD KRVESKYGPP CPPCPAPEFE GGPSVFLFPP  240
KPKDTLMISR TPEVTCVVVD VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV  300
LTVLHQDWLN GKEYKCKVSN KGLGSSIEKT ISKAKGQPRE PQVYTLPPSQ EEMTKNQVSL  360
TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSRLTVDKS RWQEGNVFSC  420
SVMHEALHNH YTQKSLSLSL GKAPASSSTK KTQLQLEHLL LALQMILNGI NNYKNPKLTE  480
MLTFKFYMPK KATELKHLQC LEEELKPLEE VLNLAQSKNF HLRPRDLISN INVIVLELKG  540
SETTFMCEYA DETATIVEFL NRWITFAQSI ISTLT                             575

SEQ ID NO: 559         moltype = AA  length = 439
FEATURE                Location/Qualifiers
source                 1..439
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 559
QVQLVESGGG VVQPGRSLRL DCKASGITFS NSGMHWVRQA PGKGLEWVAV IWYDGSKRYY  60
ADSVKGRFTI SRDNSKNTLF LQMNSLRAED TAVYYCATND DYWGQGTLVT VSSASTKGPS  120
VFPLAPCSRS TSESTAALGC LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS  180
VVTVPSSSLG TKTYTCNVDH KPSNTKVDKR VESKYGPPCP PCPAPEFLGG PSVFLFPPKP  240
KDTLMISRTP EVTCVVVDVS QEDPEVQFNW YVDGVEVHNA KTKPREEQFN STYRVVSVLT  300
VLHQDWLNGK EYKCKVSNKG LPSSIEKTIS KAKGQPREPQ VYTLPPSQEE MTKNQVSLTC  360
LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SRLTVDKSRW QEGNVFSCSV  420
MHEALHNHYT QKSLSLSLG                                               439

SEQ ID NO: 560         moltype = AA  length = 451
FEATURE                Location/Qualifiers
source                 1..451
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 560
QVQLQQPGAE LVKPGASVKM SCKASGYTFT SYNMHWVKQT PGRGLEWIGA IYPGNGDTSY  60
NQKFKGKATL TADKSSSTAY MQLSSLTSED SAVYYCARST YYGGDWYFNV WGAGTTVTVS  120
AASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG  240
GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY  300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP QVYTLPPSRD  360
ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSKLTVDKSR  420
WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K                                 451

SEQ ID NO: 561         moltype = AA  length = 450
FEATURE                Location/Qualifiers
source                 1..450
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 561
QVQLQQPGAE LVKPGASVKM SCKASGYTFT SYNMHWVKQT PGRGLEWIGA IYPGNGDTSY  60
NQKFKGKATL TADKSSSTAY MQLSSLTSED SAVYYCARST YYGGDWYFNV WGAGTTVTVS  120
AASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELAG  240
APSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY  300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP QVYTLPPSRD  360
ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSKLTVDKSR  420
WQQGNVFSCS VMHEALHNHY TQKSLSLSPG                                   450

SEQ ID NO: 562         moltype = AA  length = 213
FEATURE                Location/Qualifiers
source                 1..213
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 562
QIVLSQSPAI LSASPGEKVT MTCRASSSVS YIHWFQQKPG SSPKPWIYAT SNLASGVPVR  60
FSGSGSGTSY SLTISRVEAE DAATYYCQQW TSNPPTFGGG TKLEIKRTVA APSVFIFPPS  120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL  180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC                               213

SEQ ID NO: 563         moltype = AA  length = 580
FEATURE                Location/Qualifiers
source                 1..580
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 563
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELAGAPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
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NVFSCSVMHE ALHNHYTQKS LSLSPGKAPA SSSTKKTQLQ LEHLLLDLQM ILNGINNYKN  480
PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR DLISNINVIV  540
LELKGSETTF MCEYADETAT IVEFLNRWIT FAQSIISTLT                        580

SEQ ID NO: 564         moltype = AA  length = 456
FEATURE                Location/Qualifiers
source                 1..456
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 564
EVQLQESGPG LVKPSQSLSL TCSVTGYSIT SSYRWNWIRK FPGNRLEWMG YINSAGISNY  60
NPSLKRRISI TRDTSKNQFF LQVNSVTTED AATYYCARSD NMGTTPFTYW GQGTLVTVSS  120
AKTTPPSVYP LAPGCGDTTG SSVTLGCLVK GYFPESVTVT WNSGSLSSSV HTFPALLQSG  180
LYTMSSSVTV PSSTWPSQTV TCSVAHPASS TTVDKKLEPS GPISTINPCP PCKECHKCPA  240
PNLEGGPSVF IFPPNIKDVL MISLTPKVTC VVVDVSEDDP DVQISWFVNN VEVHTAQTQT  300
HREDYASTIR VVSTLPIQHQ DWMSGKEFKC KVNNKDLPSP IERTISKIKG LVRAPQVYIL  360
PPPAEQLSRK DVSLTCLVVG FNPGDISVEW TSNGHTEENY KDTAPVLDSD GSYFIYSKLN  420
MKTSKWEKTD SFSCNVRHEG LKNYYLKKTI SRSPGK                            456

SEQ ID NO: 565         moltype = AA  length = 595
FEATURE                Location/Qualifiers
source                 1..595
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 565
EVQLQESGPG LVKPSQSLSL TCSVTGYSIT SSYRWNWIRK FPGNRLEWMG YINSAGISNY  60
NPSLKRRISI TRDTSKNQFF LQVNSVTTED AATYYCARSD NMGTTPFTYW GQGTLVTVSS  120
AKTTPPSVYP LAPGCGDTTG SSVTLGCLVK GYFPESVTVT WNSGSLSSSV HTFPALLQSG  180
LYTMSSSVTV PSSTWPSQTV TCSVAHPASS TTVDKKLEPS GPISTINPCP PCKECHKCPA  240
PNLEGGPSVF IFPPNIKDVL MISLTPKVTC VVVDVSEDDP DVQISWFVNN VEVHTAQTQT  300
HREDYASTIR VVSTLPIQHQ DWMSGKEFKC KVNNKDLPSP IERTISKIKG LVRAPQVYIL  360
PPPAEQLSRK DVSLTCLVVG FNPGDISVEW TSNGHTEENY KDTAPVLDSD GSYFIYSKLN  420
MKTSKWEKTD SFSCNVRHEG LKNYYLKKTI SRSPGKSGGG GSAPTSSSTK KTQLQLEHLL  480
LDLQMILNGI NNYKNPKLTR MLTKKFRMPK KATELKHLQC LEEELKPLEE RLNLAQSKNF  540
HLRPRDLISN INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT       595

SEQ ID NO: 566         moltype = AA  length = 218
FEATURE                Location/Qualifiers
source                 1..218
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 566
DIVMTQGTLP NPVPSGESVS ITCRSSKSLL YSDGKTYLNW YLQRPGQSPQ LLIYWMSTRA  60
SGVSDRFSGS GSGTDFTLKI SGVEAEDVGI YYCQQGLEFP TFGGGTKLEL KRADAAPTVS  120
IFPPSSEQLT SGGASVVCFL NNFYPKDINV KWKIDGSERQ NGVLNSWTDQ DSKDSTYSMS  180
STLTLTKDEY ERHNSYTCEA THKTSTSPIV KSFNRNEC                          218

SEQ ID NO: 567         moltype = AA  length = 455
FEATURE                Location/Qualifiers
source                 1..455
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 567
EVQLVESGGG LVQPGRSLKL SCAASGFTFG DYSMAWVRQA PKRGLEWVAN IIYDGSRTFY  60
RDSVKGRFTI SRDNAKPTLY LQMDSLRPED TATYYCATHN YPGYAMEAWG QGTSVTVSSA  120
KTTPPSVYPL APGCGDTTGS SVTLGCLVKG YFPESVTVTW NSGSLSSSVH TFPALLQSGL  180
YTMSSSVTVP SSTWPSQTVT CSVAHPASST TVDKKLEPSG PISTINPCPP CKECHKCPAP  240
NLEGGPSVFI FPPNIKDVLM ISLTPKVTCV VVDVSEDDPD VQISWFVNNV EVHTAQTQTH  300
REDYASTIRV VSTLPIQHQD WMSGKEFKCK VNNKDLPSPI ERTISKIKGL VRAPQVYILP  360
PPAEQLSRKD VSLTCLVVGF NPGDISVEWT SNGHTEENYK DTAPVLDSDG SYFIYSKLNM  420
KTSKWEKTDS FSCNVRHEGL KNYYLKKTIS RSPGK                             455

SEQ ID NO: 568         moltype = AA  length = 213
FEATURE                Location/Qualifiers
source                 1..213
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 568
DTVLTQSPAL PVSLGQRVNI SCRATKSVSR YVHWYQQKSG QQPRLLIYTT SNLESGVPSR  60
FSGSGSGTDF TLTIDPVEAD DIANYYCQQS NEIPYTFGAG TKLELKRADA APTVSIFPPS  120
SEQLTSGGAS VVCFLNNFYP KDINVKWKID GSERQNGVLN SWTDQDSKDS TYSMSSTLTL  180
TKDEYERHNS YTCEATHKTS TSPIVKSFNR NEC                               213

SEQ ID NO: 569         moltype = AA  length = 594
FEATURE                Location/Qualifiers
source                 1..594
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 569
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EVQLVESGGG LVQPGRSLKL SCAASGFTFG DYSMAWVRQA PKRGLEWVAN IIYDGSRTFY  60
RDSVKGRFTI SRDNAKPTLY LQMDSLRPED TATYYCATHN YPGYAMEAWG QGTSVTVSSA  120
KTTPPSVYPL APGCGDTTGS SVTLGCLVKG YFPESVTVTW NSGSLSSSVH TFPALLQSGL  180
YTMSSSVTVP SSTWPSQTVT CSVAHPASST TVDKKLEPSG PISTINPCPP CKECHKCPAP  240
NLEGGPSVFI FPPNIKDVLM ISLTPKVTCV VVDVSEDDPD VQISWFVNNV EVHTAQTQTH  300
REDYASTIRV VSTLPIQHQD WMSGKEFKCK VNNKDLPSPI ERTISKIKGL VRAPQVYILP  360
PPAEQLSRKD VSLTCLVVGF NPGDISVEWT SNGHTEENYK DTAPVLDSDG SYFIYSKLNM  420
KTSKWEKTDS FSCNVRHEGL KNYYLKKTIS RSPGKSGGGG SAPTSSSTKK TQLQLEHLLL  480
DLQMILNGIN NYKNPKLTRM LTKKFRMPKK ATELKHLQCL EEELKPLEER LNLAQSKNFH  540
LRPRDLISNI NVIVLELKGS ETTFMCEYAD ETATIVEFLN RWITFCQSII STLT        594

SEQ ID NO: 570         moltype = AA  length = 595
FEATURE                Location/Qualifiers
source                 1..595
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 570
EVQLVGSGGG LVQPGGSLKL SCAASGFTFS DFYMAWVRQA PTKGLEWVAS ISTGGGNTHY  60
RDSVKGRFTI SRDNAKSTLY LQMDSLRSEE TATYYCARLL STISTPFDYW GQGVIVTVSS  120
AKTTPPSVYP LAPGCGDTTG SSVTLGCLVK GYFPESVTVT WNSGSLSSSV HTFPALLQSG  180
LYTMSSSVTV PSSTWPSQTV TCSVAHPASS TTVDKKLEPS GPISTINPCP PCKECHKCPA  240
PNLEGGPSVF IFPPNIKDVL MISLTPKVTC VVVDVSEDDP DVQISWFVNN VEVHTAQTQT  300
HREDYASTIR VVSTLPIQHQ DWMSGKEFKC KVNNKDLPSP IERTISKIKG LVRAPQVYIL  360
PPPAEQLSRK DVSLTCLVVG FNPGDISVEW TSNGHTEENY KDTAPVLDSD GSYFIYSKLN  420
MKTSKWEKTD SFSCNVRHEG LKNYYLKKTI SRSPGKSGGG GSAPTSSSTK KTQLQLEHLL  480
LDLQMILNGI NNYKNPKLTR MLTKKFRMPK KATELKHLQC LEEELKPLEE RLNLAQSKNF  540
HLRPRDLISN INVIVLELKG SETTFMCEYA DETATIVEFL NRWITFCQSI ISTLT       595

SEQ ID NO: 571         moltype = AA  length = 214
FEATURE                Location/Qualifiers
source                 1..214
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 571
DVVLIQSPTT LSVTPGETVS LSCRASHSVG TNLHWYQQRT NESPSLLIKY SSHSTSGIPS  60
RFSATGSGTD FTLNISNVEF DDVASYFCQQ SQKWPLTFGS GTKLEIKRAD AAPTVSIFPP  120
SSEQLTSGGA SVVCFLNNFY PKDINVKWKI DGSERQNGVL NSWTDQDSKD STYSMSSTLT  180
LTKDEYERHN SYTCEATHKT STSPIVKSFN RNEC                              214

SEQ ID NO: 572         moltype = AA  length = 591
FEATURE                Location/Qualifiers
source                 1..591
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 572
EVQLQQSGPE LVKPGASVKI SCKTSGYTFT EYTMHWVKQS HGKSLEWIGG INPNNGGTTY  60
NQKFKGKATL TVDKSSSTAY MELRSLTSQD SAVYYCARDY YRYGHYYAMD YWGQGTSVTV  120
SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
SSGLYSLSSV VTVPSSSLGT QTYICNVNHK PSNTKVDKKV EPKSCDKTHT CPPCPAPELL  240
GGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ  300
YNSTYRVVSV LTVLHQDWLN GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR  360
DELTKNQVSL TCLVKGFYPS DIAVEWESNG QPENNYKTTP PVLDSDGSFF LYSKLTVDKS  420
RWQQGNVFSC SVMHEALHNH YTQKSLSLSP GKSGGGGSAP TSSSTKKTQL QLEHLLLDLQ  480
MILNGINNYK NPKLTRMLTF KFYMPKKATE LKHLQCLEEE LKPLEEVLNL AQSKNFHLRP  540
RDLISNINVI VLELKGSETT FMCEYADETA TIVEFLNRWI TFCQSIISTL T           591

SEQ ID NO: 573         moltype = AA  length = 213
FEATURE                Location/Qualifiers
source                 1..213
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 573
QIVLTQSPAI MSASPGEKVT MTCSVSSSVR FMHWYQQKSG TSPKRWIYDT SKLASGVPAR  60
FSGSGSGTSY SLTISSMEAE DAATYYCQQW SSNPPTFGGG TKLKIKRTVA APSVFIFPPS  120
DEQLKSGTAS VVCLLNNFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL  180
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC                               213

SEQ ID NO: 574         moltype = AA  length = 133
FEATURE                Location/Qualifiers
source                 1..133
                       mol_type = protein
                       organism = Synthetic construct
SEQUENCE: 574
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TAKFAMPKKA TELKHLQCLE  60
EELKPLEEVL NGAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                     133

SEQ ID NO: 575         moltype = AA  length = 133
FEATURE                Location/Qualifiers
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source 1..133
mol_type = protein
organism = Synthetic construct

SEQUENCE: 575
APTSSSTKKT QLQLEALLLD LQMILNGINN YKNPKLTRML TAKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 576 moltype = AA length = 448
FEATURE Location/Qualifiers
source 1..448
mol_type = protein
organism = Synthetic construct

SEQUENCE: 576
EVQLLESGGG LVQPGGSLRL SCVGSGFNLK DYCMTWVRQA PGKGLEWVSA IVYSGGSTYY 60
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SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP 240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSQ EDPEVQFNWY VDGVEVHNAK TKPREEQFNS 300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM 360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ 420
EGNVFSCSVM HEALHNHYTQ KSLSLSLG 448

SEQ ID NO: 577 moltype = AA length = 448
FEATURE Location/Qualifiers
source 1..448
mol_type = protein
organism = Synthetic construct

SEQUENCE: 577
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SSGLYSLSSV VTVPSSSLGT KTYTCNVDHK PSNTKVDKRV ESKYGPPCPP CPAPEFLGGP 240
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TYRVVSVLTV LHQDWLNGKE YKCKVSNKGL PSSIEKTISK AKGQPREPQV YTLPPSQEEM 360
TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS RLTVDKSRWQ 420
EGNVFSCSVM HEALHNHYTQ KSLSLSLG 448

SEQ ID NO: 578 moltype = AA length = 446
FEATURE Location/Qualifiers
source 1..446
mol_type = protein
organism = Synthetic construct

SEQUENCE: 578
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GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG 420
NVFSCSVMHE ALHNHYTQKS LSLSLG 446

SEQ ID NO: 579 moltype = AA length = 218
FEATURE Location/Qualifiers
source 1..218
mol_type = protein
organism = Synthetic construct

SEQUENCE: 579
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IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS 180
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC 218

SEQ ID NO: 580 moltype = DNA length = 9868
FEATURE Location/Qualifiers
source 1..9868
mol_type = other DNA
organism = Synthetic construct

SEQUENCE: 580
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SEQ ID NO: 581 moltype = AA length = 133

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source                  1..133
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WITFCQSIIS TLT                                                     133

SEQ ID NO: 582          moltype = AA  length = 585
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SSASTKGPSV FPLAPSSKST SGGTAALGCL VKDYFPEPVT VSWNSGALTS GVHTFPAVLQ  180
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SEQ ID NO: 583          moltype = AA  length = 216
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SEQ ID NO: 584          moltype = AA  length = 290
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source                  1..290
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MRIFAVFIFM TYWHLLNAFT VTVPKDLYVV EYGSNMTIEC KFPVEKQLDL AALIVYWEME  60
DKNIIQFVHG EEDLKVQHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG  120
ADYKRITVKV NAPYNKINQR ILVVDPVTSE HELTCQAEGY PKAEVIWTSS DHQVLSGKTT  180
TTNSKREEKL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAELVIPELP LAHPPNERTH  240
LVILGAILLC LGVALTFIFR LRKGRMMDVK KCGIQDTNSK KQSDTHLEET              290

SEQ ID NO: 585          moltype = AA  length = 447
FEATURE                 Location/Qualifiers
source                  1..447
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 585
EVQLVGSGGG LVQPGGSLKL SCAASGFTFS DFYMAWVRQA PTKGLEWVAS ISTGGGNTHY  60
RDSVKGRFTI SRDNAKSTLY LQMDSLRSEE TATYYCARLL STISTPFDYW GQGVIVTVSS  120
ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  180
GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS SIEKTISKAK GQPREPQVYT LPPSQEEMTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG  420
NVFSCSVMHE ALHNHYTQKS LSLSLGK                                      447

SEQ ID NO: 586          moltype = AA  length = 214
FEATURE                 Location/Qualifiers
source                  1..214
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 586
DVVLIQSPTT LSVTPGETVS LSCRASHSVG TNLHWYQQRT NESPSLLIKY SSHSTSGIPS  60
RFSATGSGTD FTLNISNVEF DDVASYFCQQ SQKWPLTFGS GTKLEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 587          moltype = AA  length = 770
FEATURE                 Location/Qualifiers
source                  1..770
                        mol_type = protein
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organism = Synthetic construct

SEQUENCE: 587

EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LAHLLLDLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 588 moltype = AA length = 770

FEATURE Location/Qualifiers

source 1..770

mol_type = protein

organism = Synthetic construct

SEQUENCE: 588

EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLILQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 589 moltype = AA length = 770

FEATURE Location/Qualifiers

source 1..770

mol_type = protein

organism = Synthetic construct

SEQUENCE: 589

EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLSLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 590 moltype = AA length = 770

FEATURE Location/Qualifiers

source 1..770

mol_type = protein

organism = Synthetic construct

SEQUENCE: 590

EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLHLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 591 moltype = AA length = 770

FEATURE Location/Qualifiers

source 1..770

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                    mol_type = protein
                    organism = Synthetic construct
SEQUENCE: 591
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN  480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE  540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC  600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLWLQM  660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR  720
DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT              770

SEQ ID NO: 592         moltype = AA  length = 770
FEATURE                Location/Qualifiers
source                 1..770
                    mol_type = protein
                    organism = Synthetic construct
SEQUENCE: 592
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN  480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE  540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC  600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLYLQM  660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR  720
DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT              770

SEQ ID NO: 593         moltype = AA  length = 770
FEATURE                Location/Qualifiers
source                 1..770
                    mol_type = protein
                    organism = Synthetic construct
SEQUENCE: 593
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN  480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE  540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC  600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLRLQM  660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR  720
DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT              770

SEQ ID NO: 594         moltype = AA  length = 770
FEATURE                Location/Qualifiers
source                 1..770
                    mol_type = protein
                    organism = Synthetic construct
SEQUENCE: 594
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN  480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE  540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC  600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLFLQM  660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR  720
DLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT              770

SEQ ID NO: 595         moltype = AA  length = 770
FEATURE                Location/Qualifiers
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source 1..770
mol_type = protein
organism = Synthetic construct

SEQUENCE: 595
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
KLISNINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 596 moltype = AA length = 770
FEATURE Location/Qualifiers
source 1..770
mol_type = protein
organism = Synthetic construct
SEQUENCE: 596
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLIANINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 597 moltype = AA length = 770
FEATURE Location/Qualifiers
source 1..770
mol_type = protein
organism = Synthetic construct
SEQUENCE: 597
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLISYINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 598 moltype = AA length = 770
FEATURE Location/Qualifiers
source 1..770
mol_type = protein
organism = Synthetic construct
SEQUENCE: 598
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLISDINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 599 moltype = AA length = 770

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FEATURE                 Location/Qualifiers
source                  1..770
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 599
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN  480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE  540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC  600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM  660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR  720
DLISRINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT              770

SEQ ID NO: 600          moltype = AA  length = 770
FEATURE                 Location/Qualifiers
source                  1..770
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 600
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN  480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE  540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC  600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM  660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR  720
DLISEINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT              770

SEQ ID NO: 601          moltype = AA  length = 770
FEATURE                 Location/Qualifiers
source                  1..770
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 601
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN  480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE  540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC  600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM  660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR  720
DLISFINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT              770

SEQ ID NO: 602          moltype = AA  length = 770
FEATURE                 Location/Qualifiers
source                  1..770
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 602
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY  60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST  120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY  180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV  240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY  300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK  360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG  420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN  480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE  540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC  600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM  660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR  720
DLISIINVIV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT              770
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SEQ ID NO: 603 moltype = AA length = 770
FEATURE Location/Qualifiers
source 1..770
mol_type = protein
organism = Synthetic construct
SEQUENCE: 603
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RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLISNINVAV LELKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 604 moltype = AA length = 770
FEATURE Location/Qualifiers
source 1..770
mol_type = protein
organism = Synthetic construct
SEQUENCE: 604
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLISNINVIV LALKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 605 moltype = AA length = 770
FEATURE Location/Qualifiers
source 1..770
mol_type = protein
organism = Synthetic construct
SEQUENCE: 605
EVQLVESGGG LVQPGRSLKL SCAVSGFTFS DYAMAWVRQA PKKGLEWVAT ISYDGSRTYY 60
RDSVKGRFTI SRDNAKITLY LQMDSLRSED TATYYCARHG SGYFDYWGQG VMVTVSSAST 120
KGPSVFPLAP SSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 180
SLSSVVTVPS SSLGTQTYIC NVNHKPSNTK VDKKVEPKSC DKTHTCPPCP APELLGGPSV 240
FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY 300
RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK 360
NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG 420
NVFSCSVMHE ALHNHYTQKS LSLSPGKSGG GGSELCDDDP PEIPHATFKA MAYKEGTMLN 480
CECKRGFRRI KSGSLYMLCT GNSSHSSWDN QCQCTSSATR NTTKQVTPQP EEQKERKTTE 540
MQSPMQPVDQ ASLPGHCREP PPWENEATER IYHFVVGQMV YYQCVQGYRA LHRGPAESVC 600
KMTHGKTRWT QPQLICTSGG GGSGGGGSGG GGSGGGSAPT SSSTKKTQLQ LEHLLLDLQM 660
ILNGINNYKN PKLTRMLTFK FYMPKKATEL KHLQCLEEEL KPLEEVLNLA QSKNFHLRPR 720
DLISNINVIV LKLKGSETTF MCEYADETAT IVEFLNRWIT FCQSIISTLT 770

SEQ ID NO: 606 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct
SEQUENCE: 606
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EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

SEQ ID NO: 607 moltype = AA length = 133
FEATURE Location/Qualifiers
source 1..133
mol_type = protein
organism = Synthetic construct
SEQUENCE: 607
APTSSSTKKT QLQLEHLLLN LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE 60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR 120
WITFCQSIIS TLT 133

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SEQ ID NO: 608          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 608
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EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 609          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 609
APTSSSTKKT QLQLEHLLLE LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 610          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 610
APTSSSTKKT QLQLEHLLLG LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 611          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 611
APTSSSTKKT QLQLEHLLLI LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 612          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 612
APTSSSTKKT QLQLEHLLLL LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 613          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 613
APTSSSTKKT QLQLEHLLLK LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 614          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 614
APTSSSTKKT QLQLEHLLLM LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 615          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 615
APTSSSTKKT QLQLEHLLLF LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
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WITFCQSIIS TLT                                                    133

SEQ ID NO: 616          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 616
APTSSSTKKT QLQLEHLLLP LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 617          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 617
APTSSSTKKT QLQLEHLLLT LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 618          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 618
APTSSSTKKT QLQLEHLLLW LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 619          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 619
APTSSSTKKT QLQLEHLLLY LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 620          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Synthetic construct
SEQUENCE: 620
APTSSSTKKT QLQLEHLLLV LQMILNGINN YKNPKLTEML TFKFYMPKKA TELKHLQCLE  60
EELKPLEEVL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133

SEQ ID NO: 621          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 621
APTSSSTKKT QLQLEHLLLD LQMILNGINN YKNPKLTRML TKKFRMPKKA TELKHLQCLE  60
EELKPLEERL NLAQSKNFHL RPRDLISNIN VIVLELKGSE TTFMCEYADE TATIVEFLNR  120
WITFCQSIIS TLT                                                    133
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What is claimed:

1. An anti-human PD-1 (hPD-1) antibody-modified human interleukin-2 (hIL-2) immunoconjugate comprising:

a modified hIL-2 protein comprising the amino acid sequence of SEQ ID NO: 217; and

an anti-hPD-1 antibody, or antigen-binding fragment thereof, that immunospecifically binds to hPD-1, wherein the antibody or antigen-binding fragment thereof, comprises a heavy chain complementarity determining region 1 (CDR1) comprising the amino acid sequence of SEQ ID NO: 418, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO: 419, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO: 420, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO: 421, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO: 422, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO: 423.

2. The immunoconjugate of claim **1**, wherein the anti-hPD-1 antibody, or antigen-binding fragment thereof, comprises an IgG1 heavy chain constant region.

3. The immunoconjugate of claim **2**, wherein the anti-hPD-1 antibody, or antigen-binding fragment thereof, comprises an L235A substitution and a G237A substitution, according to EU numbering.

4. The immunoconjugate of claim **3**, wherein the anti-hPD-1 antibody, or antigen-binding fragment thereof, com-

prises a heavy chain (HC) comprising the amino acid sequence of SEQ ID NO: 414 and a light chain (LC) comprising the amino acid sequence of SEQ ID NO: 415.

5. An anti-hPD-1 antibody-modified hIL-2 immunoconjugate comprising:

a modified hIL-2 protein comprising the amino acid sequence of SEQ ID NO: 217; and

an anti-hPD-1 antibody, or antigen-binding fragment thereof, comprising a VH comprising the amino acid sequence of SEQ ID NO: 416 and a VL comprising the amino acid sequence of SEQ ID NO: 417.

6. The immunoconjugate of claim **5**, wherein the anti-hPD-1 antibody, or antigen-binding fragment thereof, comprises an IgG1 heavy chain constant region.

7. The immunoconjugate of claim **6**, wherein the anti-hPD-1 antibody, or antigen-binding fragment thereof, comprises an L235A substitution and a G237A substitution, according to EU numbering.

8. The immunoconjugate of claim **7**, wherein the anti-hPD-1 antibody, or antigen-binding fragment thereof, comprises a HC comprising the amino acid sequence of SEQ ID NO: 414 and a LC comprising the amino acid sequence of SEQ ID NO: 415.

9. An anti-hPD-1 antibody-modified hIL-2 immunoconjugate comprising:

a modified hIL-2 protein comprising the amino acid sequence of SEQ ID NO: 217; and

an anti-hPD-1 antibody, or antigen-binding fragment thereof, comprising a HC comprising the amino acid sequence of SEQ ID NO: 414 and a LC comprising the amino acid sequence of SEQ ID NO: 415.

10. The immunoconjugate of claim **9**, comprising:

a light chain comprising the amino acid sequence of SEQ ID NO: 415; and

a heavy chain-modified hIL-2 protein fusion comprising the amino acid sequence of SEQ ID NO: 532.

* * * * *